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                                                                                                   New Ehrlichia ruminantium polynucleotides, useful as vaccines for inducing protective immunity, and protecting animals or humans against rickettsial diseases, e.g. typhus, spotted fever or heart water.
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Claim 1; Page 131-133; 206pp; English

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                                                                                                                                                                   ATATTACATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACAAATT
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                                    TTACTTATTATAAAATAATATGTTTGCACACTTTTTCACTACATCATGTATATAATGAA 1920
                                                                                 ATATTACATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACAAATT 1800
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4021 TATAAAAATTAGTTACTAATTATTACTAATTTATCAAGCATAGGTTTCCTATATATCCAAA 4080	3961 C	3901 3901	3841 AATATACAATCTTTCCTTGGACATTTCAAAATCCTGTGCCATAATTACCTACAATACTAA 3900	3781 TAATATATCTTTATTAGATTTCTGATATCAACTTCATCATCAACAACTAATACTTCAGA 3840 	3721 AGCCATCTTGATCGCGGATAAACCATCAACTGCTAATTTAGTGACATAATTATCATCACT 3780 	3661 ATCAATATCAGATCCTCTTAACCATATATCCAATAATACAACATCAGGCTCTTTTTCATA 3720 	3601 AATCATAATAACAGCCAAATAAGGATACCTTTCTTTAAGCTTTTCCAGTACACTTAATCC 	3541 ATAATCATAAGCACCCATATGCAGAGACTTTACAGCAGTGGCAATATTACCATGCCCACT	3481 AGACTCTATAGCTCTCTTTACAACTAACTTTAATCTTCCTTC	3421 GACTATTTCATAATCCTCAAATGCTGATTTCAACTCATCATTTTCTCTTACGTAATCTACC 3480 3421 GACTATTTCATAATCCTCAAATGCTGATTTCAACTCATCATTTTCTCTACGTAATCTACC 3480	3361 CGATGTAGTAGCTGCTTTATTAATCATACTTCTCAAATTACGTATAACAGGGAGTTACC	3301 TATTAGCCTAGCAACTACTTCCTTTCCAACACCTGGCGAACCAGTAATGAGTATACGACT 3360	3241 TGGTAGCATAGATGAGTAGATAGATAAATGGAGTATGATACCCCTTGGATTTTTATG	3181 ATGAGACAATATATTACTTTCCTCACTACCAAATATATTAACCAAGTAATTATTAGC	3121 ATCTAFAAATAACGTACCA/GATTIGCTTGCTCTAFAATTCCAAFATGAGAGGTACTCT	3061 TCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTATCGTTACTGCTGATCTGTTACTTC 312	3001 AGACACAATAATTCTCACATCTATACTAACAGGAATCTTACTATTTTCCCTATATATTTT 3060

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ARESULT 2
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XX Ditr
OS Ehrl
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   (UYFL ) UNIV FLORIDA.
                                                                20-FEB-2001; 2001US-0269944P
                                                                                                                         20-FEB-2002; 2002WO-US005772.
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                                                                                                                                                                                                                                                                                                                   Ehrlichia ruminantium
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1416 BP; 472 A; 297 C; 161 G; 486 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Ehrlichia ruminantium polynucleotides, useful as vaccines for inducing protective immunity, and protecting animals or humans against rickettsial diseases, e.g. typhus, spotted fever or heart water.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 137-138; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-723186/78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunity to rickettsial infection, including Ehrlichia ruminantium (formerly Cowdria ruminantium). The invention also relates to novel E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 29.8%; Score 1416; DB 6; Length 1416; Local Similarity 100.0%; Pred. No. 7.3e-215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2647
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                                                                                                                                  Vaccine; immunity; rickettsial infection; spotted fever; heart water; typhus; pathogen; immunostimulant; antibacterial; 19hworf4i; gene; cell division protein; ftsQ; ds.
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                                                                                                                                                                                                                              Ehrlichia ruminantium 19hworf4i protein encoding DNA.
                                                                                        Ehrlichia ruminantium.
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                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                        BP.
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4274 AGGTAATTTTATATTTAAACCACTAGACAAAATAATATCCCÁCCAATGACTATCAACATA

AGGTAATTTTATATTTAAACCACTAGACAAAATAATATCCCACCAATGACTATCAACATA

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ATCTAGATGAGTTAACGCACCATCTCCATGTATTGAAGTCAAATCATCCCGTATATTACA

4453 .240

ATCTAGATGAGTTAACGCACCATCTCCATGTATTGAAGTCAAATCATCCCGTATATTACA

TGTGATAGATGAAACCATACCACCAACAAGAGTATTATCATTGACTACTTCACGTATAAA 4393

TGTGATAGATGAAACCÁTACCACCÁACAAGÁGTATTATCATTGACTÁCTTCÁCGTÁTAAA

ATTATCAACAATAATATGTCCAAAACTATCAATGATAGAATTTTTTGTTATCATGATACCA

ATTATCAACAATAATATGTCCAAAACTATCAATGATAGAATTTTTGTTATCATGATACCA

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TTCATTACCATCAATCAATATTTTATCAACAGTAAATCCACAATTGACTAATTGATC

AGGCACAAAAAGATAGACCTTGCATCAACAAGTTTACGTATTTCATCAGAACTTACATA

AGGCACAAAAAAGATAGACCTTGCATCAACAAGTTTACGTATTTCATCAGAACTTACATA 4693

AACTGAGGCATTTTTGATCCATGGATGACTAGACTCTATTTTGTTTCTCAAATCAGCCAA

AACTGAGGCATTTTTGATCCATGGATGACTAGACTCTATTTTGTTTCTCAAATCAGCCAA

480

4633 420 ATTTGCAAAAGCAGAATATTCTTGAACTGTTATCTGTAAAGTATTTGGTAACAGCCTCTT

4573 360 4513

ATTTGCAAAAGCAGAATATTCTTGAACTGTTATCTGTAAAGTATTTGGTAACAGCCTCTT

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                                                                                                                                                                                                                                                           immunity to rickettsial infection, including Ehrlichia ruminantium (formerly Cowdria ruminantium). The invention also relates to novel E. ruminantium polynucleotides and their corresponding proteins. Sequences of the invention are useful for inducing immunity, particularly protective immunity. They are also useful for detecting the presence of E. ruminantium in a biological sample. They are useful in vaccines for protecting animals or humans against rickettsial diseases, e.g. typhus, spotted fever or heart water. Sequences of the invention are useful for detecting antibodies to pathogens. The present sequence is a DNA encoding E. ruminantium hypothetical cell division protein (ftsQ; 19hworf4i)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 138-139; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Ehrlichia ruminantium polynucleotides, useful as vaccines for inducing protective immunity, and protecting animals or humans against rickettsial diseases, e.g. typhus, spotted fever or heart water.
                                                                                                                                                                                                                               Sequence 597 BP; 220 A; 117 C; 68 G; 192 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to nucleic acid vaccines for conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-723186/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2001; 2001US-0269944P
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                                                                                                    4154 TTATTTCATTTATATTAACCTTCCCTGGAACACGCATGTCTATAGTTTTCCATACTAAAAA 4213
                                  4214 CTCACTTGAAGCTTTATAGATATTCAATAATTCACGCCAAGCAGCATAAGAATCATTATT
                                                                                                                                                       597;
  61
                                                                           Н
                                                                                                                                                                         Similarity
                                                                           TTATTTCATTATATTAACCTTCCCTGGAACACGCATGTCTATAGTTTTCCATACTAAAAA
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L, Mwangi DM,
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mwangi
                                                                                                                                                 12.6%; Score 597; DB 6; 100.0%; Pred. No. 1.9e-85; tive 0; Mismatches 0;
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Mcguire TC,
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Mahan SM
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                                                                                                                                                                                          Length 597;
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RESULT 4
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Best Local Similarity 100.
Matches 371; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ruminantium polynucleotides and their corresponding proteins. Sequences of the invention are useful for inducing immunity, particularly protective immunity. They are also useful for detecting the presence of E. ruminantium in a biological sample. They are useful in vaccines for protecting animals or humans against rickettsial diseases, e.g. typhus, spotted fever or heart water. Sequences of the invention are useful for detecting antibodies to pathogens. The present sequence is a DNA encoding Enrichia ruminantium hypothetical integrase/recombinase (19hworfli)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Ehrlichia ruminantium polynucleotides, useful as vaccines for inducing protective immunity, and protecting animals or humans against rickettsial diseases, e.g. typhus, spotted fever or heart water.
                                                                                                                                                                                                                                                                                                                                          Sequence 371 BP; 128 A; 74 C; 45 G; 124 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to nucleic acid vaccines for conferring immunity to rickettsial infection, including Ehrlichia ruminantium (formerly Cowdria ruminantium). The invention also relates to novel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; immunity; rickettsial infection; spotted fever; heart water; typhus; pathogen; immunostimulant; integrase; recombinase; 19hworfli;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial; enzyme; gene; ds.
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                                                                               121
181 CTCAAATCTCCAATTTTAACATGCACAAGATTATTTAATGTAACAGAACACCCTGTACTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 TTCATTACCATCAATAATTTTTATCAACAGTAAATCCACAATTGACTAATTGATC 597
                                                                                                               61 GCTTGACTGTCTATATAGTACATACGTGATAGATAACGAAAAAATTTCTCAAAGCAGAC 120
                                                                                                                                                 61 GCTTGACTGTCTATATAGTACATACGTGATAGATAACGAAAAAAATTTCTCAAAAGCAGAC 120
                                                                                                                                                                                                                          AGTGACCTTGCATTGGTAACTGCTTCAACTCCACATTGATATCTAGAAGCAAACCATTT 180
                                                                                                                                                                                      AGTGACCTTGCATTGGTAACTGCTTCAACTCCACATTGATATCTAGAAGCAAACCATTTT 180
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, Mwangi DM,
                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                               7.8%; Score 371; DB 6; Length 371; 00.0%; Pred. No. 1e-49;
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Mcguire TC,
                                                                                                                                                                                                                                                                 0; Mismatches
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Mahan SM;
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                                                                                                                                                                                                                         New immunogenic polypeptide comprising epitope of Lawsonia spp. polypeptide such as fihB, fliR, ntrC, glnH, motA, polypeptides, useful in vaccines for treatment of porcine proliferative enteropathy in pigs and
                                                                                                                                                                                                                                                                                                                             Rosey EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-2001; 2001WO-AU001462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogen; fihB; fliR; ntrC; glnH; motA; motB; tlyC; ytfM; ytfN; porcine; pig; avian; bird; porcine proliferative enteropathy; PPE; intestinal adenomatosis complex; porcine intestinal adenomatosis; PIA; necrotic enteritis; proliferative haemorrhagic enteropathy; regional ileitis; haemorrhagic bowel syndrome; vaccine; antibacterial; porcine proliferative enetritis; Campylobacter spp.-induced enteritis;
                                                                                                                                                                                                                                                                                    P-PSDB; ABG68912
                                                                                                                                                                                                                                                                                                   WPI; 2002-557448/59.
                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-2000; 2000AU-00001381.
17-NOV-2000; 2000US-0249596P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK97886;
                                                                                                                                                                                                                                                                                                                                                         (AUPO-) AUSTRALIAN PORK (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; as.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding Lawsonia intracellularis antigenic ntrC protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK97886 standard; DNA; 1370 BP.
                                                                                                                                                                                                                                                                                                                                                                                    (AGRI-) AGRIC VICTORIA SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CTCAAATCTCCAATTTTAACATGCACAAGATTATTTAATGTAACAGAACACCCTGTACTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 TTATTCGACAT 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GAATACCTCTTCTCTTGTTCCATCCATATTTTCCAATTATTTACAATATCATAGAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAACTGTATTCAAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAACTGTATTCAAA
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                                                                                                                                                                                                                                                                                                                             King KW,
                                                                                                                                                                                                                                                                                                                             Good RT,
                                                                                                                                                                                                                                                                                                                             Strugnell RA;
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The invention describes an isolated or recombinant immunogenic polypeptide (I) which comprises, mimics or cross-reacts with a B-cell or T-cell epitope of a Lawsonia spp. polypeptide such as fihB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM or ytfN polypeptides. (I) is useful for identifying whether or not a porcine or avian animal has suffered from a

Claim 6; Page 104-107; 155pp; English.

past infection, or is currently infected, with Lawsonia spp or a microorganism that is immunologically cross-reactive with Lawsonia spp. Antibodies are useful for diagnosing infection of a porcine or avian animal by Lawsonia spp. or a microorganism that is immunologically cross-reactive with Lawsonia spp. A nucleic acid encoding a Lawsonia spp. or related microorganism in a biological sample derived from a porcine or related microorganism in a biological sample derived from a porcine or

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           avian animal subject. (1) is preferably useful for vaccinating porcine animals against intestinal diseases collectively known as porcine proliferative enteropathy (PPE), previously known as intestinal adenomatosis complex, porcine intestinal adenomatosis (PIA), necrotic entertitis, proliferative haemorrhagic enteropathy, regional ileitis, haemorrhagic bowel syndrome, porcine proliferative enetritis and Campylobacter spp.-induced enteritis. (1) is also useful in vaccines for the prophylaxis and treatment of PPE in birds. This sequence encodes a Lawsonia intracellularis immunogenic peptide used in the creation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1370 BP; 443 A; 201 C; 278 G; 448 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   porcine vaccine described in the invention
                                                     3259 САТАGATATAAATGGAGTATCATACCCCTTGGATTTTTTATGTATTAGCCTAGCAACTAC 3318
                                                                                                                                                                                                  3139 ATGATTTGCTTGCTCTATAATTCCAATATGAGGAGGTACTCTATGAGACAATATATTATT 3198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2719 AGGAGATTTCATAATTAAAATCCATTCTATAACATTACGTAATTGTCTTAAGTTACCTGG 2778
                                                                                                                                                                                                                                                                       2899 TTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATATAAATCCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2659 ATTAATAGGCGAATTAGATACTATATCTACTGGTAAATCTTTTGCTGTAATCATCTCCTT 2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1238 AAAAGCTATTTTAGCCTGGTTAAAATCTATATCGGGAAGAAAGTTATAATGGGAAGAAAA 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2482 ACACAATCCAAGAATTTTCAATTTACGGTGTAATGCTGAACGTTCCATTCCAACAAATTC
                                                                                              643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2602 AAATTCTTCACGAGCTTTACGTAATGGTACA---GAAATAACTTTAGCACTTAAAAACATC 2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1298 TGCTAATCGGGTAATATTTCCTTGATAAGCATGTAATTTTTCAGTTAAAAATTTTGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1358 ATAAATACCATAGCTTTTTAGCTTTCTATATAAATAACTTCTTTCAAGTCCAATAGCTTC 1299
                                                                                                                                                               698 TTTATGTGCCAACTCAAAACGACCTGCACGAGAAGCATCGGCACCAGTAAAGGCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             998 ATAACGTTTACTCAACTGAATCACAAACCTATTTAATAATAGCTCAATATCAGAATCACG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                   AACAGCTATAAATGGTTTTTGATATCGTGAGCTTCCTTTGTGCAATGCTTGTGCAGCTAA
                                                                                          -CCTTTTTCATGACCAAATAGTTCGCTTTCAATCAATTCTTCAGGGATAGCAGCACAATT 585
                                                                                                                           ACTITICCTICACTACCAAATATATTAACCAAGTAATTATTAGCTGGTAGCATAGATGAGTA 3258
                                                                                                                                                                                                                                      CAAAATTTTTGCTTGTTTTTAAACTCATATCTCCTATTTCATCAAGAAATAATGTTCC
                                                                                                                                                                                                                                                                                                          ATCAACTTTAATAGTTCTAACACTACCAATTTTTTCAAAACATTGTTCTTGCAAAATACG 759
                                                                                                                                                                                                                                                                                                                                            ATCTATACTAACAGGAATCTTACTATTTTCCCTATATATTTTTCCCTCCTGTAATAATCT 3078
                                                                                                                                                                                                                                                                                                                                                                                 AAATGTTCCATCGCTAATAGCGTCTTCAAGATTCTTATTTGTTGCTGCAATAACTCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                   AAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGAAGACACAATAATTCTCAC 3018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTTTTTACAGATGCTATTCATAAATACCTACACAATTCCGGTATATCTGTACAATA 2898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATTCATATGACTGCATTGCTATTAAAGCTTCATCACTTAATACATGAGTACACAAACC 2838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGAATAAAGAATAACCATTCGTTCTACAAAATTAAGTAATTCTCTTACATTCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCACGAAGAGGGGGAAGATGCAATGGAACACTCGTAAGCGATAATACAAATCTTGACG 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCTTGGGTAAATATTTTÄAATTGCTTTTACCTTAGGATCTGTCAAACATACTTTCTT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.5%; Score 260.4; DB 6; Length 1370; 52.1%; Pred. No. 3.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 631; Indels 19;
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                     525
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New antisense nucleic acids, useful for identifying proteins or screening
                                    P-PSDB;
                                                                                                                                                                                                06-SEP-2001; 2001US-00948993
25-OCT-2001; 2001US-0342923P
08-FEB-2002; 2002US-00072851
                                                         WPI; 2003-029926/02
                                                                                                                                                                                  06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                    21-MAR-2001; 2001US-00815242
                                                                                                                                                                                                                                                                                        21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                               WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                 drug design; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prokaryotic essential gene #10157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACA28500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACA28500 standard; DNA; 1017 BP.
                                                                                                                                              (ELIT-) ELITRA PHARM INC.
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                                      ABU24630
                                                                                        Zamudio C,
Trawick JD,
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                                                                                          Malone
Carr G
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Antisense; ds; prokaryotic essential gene; cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3736 GGATAAACCATCAACTGCTAATTTAGTGACATAATTATCATCATCACTTAATATATCTTTTAT 3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3496 CTTTACAACTAACTTTAATCTTCCTTCTGTAAAAGGCTTTTCTATATAATCATAAGCACC 3555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3556 CATATGCAGAGACTTTACAGCAGTGGCAATATTACCATGCCCACTAATCATAATAACAGG 3615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3319 ТГССТТТССААСАССТВЕСВААССАСТААТВАБТАТАСВАСТСВАТСТАСТАСТВЕСТТТ 3378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 --GAAGCCAAATATCAAGAAAAACAAGATCTGGAGACTCTACATCAACACACTTAAGTCC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 TAATTCCTGATGAAGAGCCTGAATATGGTCTAAAGCCATAAGACCATCCCATCCCAG---- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 TTGACGGATAGCTGTTACAGCAGTTTCAATTGTGGCATGACCTGAAATCATAATAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 TGATAATAAACTTTTAAATTTTAAGATÄÄCÄGGAGÄCTGTCCTÄTAÄACTCÄCTCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 CTCTTTACCTGTACCATTCTCTCCTGTAAGTACCCAAGCATCTGTTGGAGCGACCTG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 T-GARATCTAATAGAGTCTTCATCATCTATAATAAGTA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTTCTGCTGAAGCTCTTTCTAAAACTTCATGGCCCTCATCTTCAAAAATTCCTTTCAA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTAACCATATATCCAATAATACAACATCAGGCTCTTTTTCATAAGCCATCTTGATCGC 3735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAATAAGGATACCTTTCTTTAAGCTTTTCCAGTACACTTAATCCATCAATATCAGATCC 3675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTAGCTGTAATAAGGACTTTTTCCAAAGAAAGAGGCTTTTCAATAAAATCATAAGCACC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTAATACAGTACGTAATTTGTTTTTCCCTTCTTAATCTTACTGTTTCTATAGCTCT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTATTTCATAATCCTC 3438
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Haselbeck R, Yamamoto R,
Forsyth
Ohlsen KL,
Forsyth RA,
    Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated conciding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated collypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway correspond to a proliferation, or that inhibits cellular proliferation or the compound that influences the activity of a gene on which a proliferation are required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an operanism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an operanism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an operanism of an organism. The antisense nucleic acids are useful for which each of the strains is present in a culture or collection of compound to activity of the target of a compound that inhibits the extent of the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, C. Interest of the printed specification, but was obtained in the target prokaryotic essential genes. Note: The sequence data for this patent did celectronic format directly from WIPO at the carenas obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1017 BP; 412 A; 106 C; 229 G; 270 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; SEQ ID NO 16370; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
1055 GAAATTGCAGAACATCTTCCTTGTAGTATAAGTACTTGCTGGTGATAATAAAGAACTTGGT 1114
                                                                               382 ATAAAAGAAGAACTGCCTAATAATCCTATAGTAGTATTGTCAGGCCCTAGCCATGCAGAG 441
                                                                                                                         995 GCAGAAGAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGCTAAA 105
                                                                                                                                                                           322 ATÄÄTÄGTÄÄGTATAGCTÄÄÄĠĠTÄŤÄGÄÄGAGGGTGĊÄGGGÄÄÄAGGTTATCAGÄGGTC 381
                                                                                                                                                                                                                                                                           268 CATGTGATAAGACAGGTATGCAAAAAGATAC-----AACCTTTTATAAAAGAAAATCAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AAAAAAGAAATATÄAAATATTTÄCCTAAAGTAGTAATÄCCTGCAGGGGTAAAAGCTTAT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 CATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 AAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 AAAGGATTGAAAGTTAACATATGGCATAGAAATAATAACATAGTAGAGGATATAAATATC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                           CCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAATA 994
                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACA 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATACCAACC 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGTTTGTTTTTAGGAGCAGGTAGTTTTGGAACAGCTTTAGCTGTAATGCTAGGAAAA 90
                                                                                                                                                                                                                                                                                                                                                                             AATGAAATAGAAAAAAGTATA---GAACAATGTGAATTTATAGTATTAGCAGTACCTTCC 267
                                                                                                                                                                                                                                                                                                                          CAACAATTACGCACCATATGTACACAAATACAACACAAACAGCATATGTGTAAAAAATACT 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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       Claim
                                                    distinguishes between methylated and non-methylated CpG
                                                                          Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that
                                                                                                                                                      WPI; 2003-018942/01.
                                                                                                                                                                                                   Schwope I,
                                                                                                                                                                                                                      Berlin K, Braun A, Distler J, Guetig D, Howe A, Muelle:
Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Le
Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto
                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002; 2002WO-EP003401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; haematopoietic cell proliferation disorder; cytostatic;
gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haematopoietic cell proliferation disorder related DNA sequence #386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ10246 standard; DNA; 8056 BP.
                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2001; 2001US-0278333P
                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1415 GGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTT 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1355 TCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTT 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   682 ATAATAAGA-----ATAGGTACAAAGCTTGGAGGTAAACAGGAAACTTTTTCAGGTCTT 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  856 GTAGAGGGAATAAAAGCTTGTAAAGCCTTTTATACATTAAAAGAAAAGCTAGATGTAGAA 915
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     28; SEQ ID NO 386; 117pp; English
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Best Local Similarity 43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which distinguishes between methylated and non-methylated CpG dinucleotides within the target nuclecides equences from the present specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders allowing for improved and informed treatment of patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 CAAATTTATTATACTACTCATCATATTTAGCATAATATCACATCTGACATGATTAACAAT 547
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  ATAACAAAAA----
                                        ACACACAAACAGCATATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGA 963
                                                                                       CAATACATGTATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAAT 903
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                     1984 TATTTACTACGTAATATTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACAT 2043
                                                                                                             1924 ААТТІТАСАТАААЛААСТААТААААДААССААТАСАТАТАТТАААТТАСТААААСАСС 1983
                                                                                                                                                                                                                                          1804 ATCTCCTATCTCAATTAACCAATTGTTATCAGATTATAAATTAAGTCAAATTAAACTTTTA 1863
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                   WO200277183-A2
                                                                                                                                                                                                                                                                                                                                            Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                    drug design; gene
                                                                                                                                                                                                                                                                                                                                                                              Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                       Prokaryotic essential gene #11140.
                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACA29483 standard; DNA; 1029 BP.
                      Claim 14; SEQ ID NO 17353; 1766pp; English
                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                          WPI; 2003-029926/02.
                                                                                                                                                                     (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                             06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4607 CICTATTITGTTTCTCAAAT 4626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4487 GATAGAATTTTTGTTATCATGATACCAATTTGCAAAAGCAGAATATTCTTGAACTGTTAT 4546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4307 AATATCCCACCAATGACTATCAACATATGTGATAGATGAAACCATACCACCAACAAGAGT 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4247 АССССААССАСАТААСААТСАТТАТТАССТААТТТАТАТТТАЛАССАССТАСАСААААТ 4306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4427 TGAAGTCAAATCATCCCGTATATTACAATTATCAACAATAATATGTCCAAAACTATCAAT 4486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 TTAAATTTTAAATTATAAAT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU25613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTAAAGTATTTGGTAACAGCCTCTTAACTGAGGCATTTTTGATCCATGGATGACTAGA 4606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTATCATTGACTACTTCACGTATAAAATCTAGATGAGTTAACGCACCATCTCCATGTAT 4426
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                 Malone C,
Carr GJ,
                                                                                                                                 Haselbeck R, Yamamoto R,
                                                                                                                                 Ohlsen KL,
Forsyth RA,
                                                                                                                                 Zyskind
Xu HH;
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The invention relates to an isolated nucleic acid comprising any

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for cc proliferation; (7) identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) consider the proliferation or that inhibits cellular proliferation; (8) creativaty agene or its gene product lies or a gene or which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene creative product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of confict that inhibits the creativity in proliferation to isolate candidate molecular acids are useful for identifying proteins or screening for homologous nucleic acids required crequired for proliferation in cells other than S. aureus, S. typhimurium, C. prolumental genes. Note: The sequence is one of the target processed in this patent did creation into intended specification, but was obtained in cells for monoic format directly from WIPO at one content in this patent did creation into intended specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 483; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoteer operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of inhibited.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1029 BP; 395 A; 118 C; 232 G; 284 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                          1114 TGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATATCCATCAAGATAT 1173
                                                                                                                                                                                                                                                                                                  994 AGCAGAAGAATTTTACAATATAATCCAATTTTATACTCTCTGGTCCAAGTTTTGCTAA 1053
                                                                                                                                                                                                                                                                                                                                                                                                                          934 TCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAAT 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814 CAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTAC 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       754 TTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAAC 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               694 ACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACAC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      634 GAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGC 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 AAAAGGTAATGTGAGCATGTGGACTCGAAAAGGAGGAACAAGCTAAAAAAATAAACAG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 GAAAGTATGTGTATTAGGTACTGGAAGCTGGGGAAGTGCATTAGCTTTAGGGGCTTGCAAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
ACAGATGATACAAGATTTGTTTATGAGCCCTAAACTTAGAGTTTATACGAATCCAGACAT
                                                                                                                       AGAAGTAGCAAGGGATATTCCTACTACCGTAGTAGTTGCTTCTAAAGATTTAAAAATAGC 488
                                                                                                                                                                           AGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGG 1113
                                                                                                                                                                                                                                           CTGTGAAGAAGTTACCACAAAATCCATATGTAATACTATCTGGGCCATCTCATGCTGA 428
                                                                                                                                                                                                                                                                                                                                                                AGTTATTGTTAATGTAGCTAAAGGTCTTGAAAAAGGGACTGGGCTTAGATTATCACAAGT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAGGCTGTAAGAAGTACTTGCCAAAAAATA----AAACCATTTATAAAAGAAGGACA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAACAATTACGCACCATATGTACACAAATACAACACAACAGCATATGTGTAAAAATAC 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACTGATATAGAAAAAACTATAAAAAGATTGTAAGGTA---ATAGTTTTAGCAGTTCCATC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACTAAAGAAATACAGACTATTTACCAGGAGTATTATTTCCAAATAATATAACTATAAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.7%; Score 175.2; DB 7; Length 1029; 51.6%; Pred. No. 9.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 438;
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06-2001; 2001US-0948991.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA47630 standard; DNA; 996 BP
The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus haemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prokaryotic essential gene #29287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACA47630
                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                    Claim 14; SEQ ID NO 35500; 1766pp; English.
                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1174 TATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAAT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1534 ACTACCAATTTGCATATCTATTTACAATTTATTACA 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1414 TGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCT 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1354 ATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTT 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1294 - ДАТТАЛАЛАСАСТАТАТАТАБСАЛЛАЛАЛАТСАТТСЛАТАБАТСТТСАТАСАТТЛАТТGGTCC - 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      design; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903 TATGCCTATAACTAATGCTATATATTCTGTAATAAA 938
                                                                                                                                       ABU43760.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGAGCAGACTTGGAATTGC-----TATGGGAGCTAATATGTCTACCTTTGCAGGTCT 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACGGATTAGGGTATGGTGATAATGCAAAAGCTGCCCTTATGACAAGAGGTATTAGTGA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTGGAGTAGÁACTTGGÁGGAGCATTÁÁAAAÁTÁTTÁTAGCÁTTTGGÁGCTGGGÁTÁTG 608
                                                                                                                                                                            Zamudio C,
Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACCTTAATGTAGA 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                            Haselbeck R, Yamamoto R,
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Forsyth RA,
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Xu HH;
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1175 ATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATC 1234
                                                                                                427
                                        AAACTGATTCAAGATTTATTTATGAATGATTATTTACGTGTATACACTAATAATGATTTA 546
                                                                                                                                                                                                                                                                                                                  AGTGATATTAAAGAAGCCGCGAATTTTACTGATATATATTTAATGGCTCTACCAACTAAA 246
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CC (1) a vector comprising a promoter operably linked to the nucleic acid CC encoding_a polypeptide whose expression is inhibited by the antisense condition acid; (2) a host cell containing the vector; (3) an isolated completed acid; (2) a host cell containing the vector; (3) an isolated completed or its fragment whose expression is inhibited by the containing completed for its fragment whose expression is inhibited by the containing completed or its fragment whose expression is inhibited by the containing completed for proliferation or the activity of a gene in an operan required for proliferation, (7) identifying a compound that inhibite proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which hat best compound that inhibits proliferation; (8) compound so activity; (11) a culture dependent proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound is a crivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the contiferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational contiferation to isolate candidate molecules for rational continuation to isolate candidate molecules for rational continuation and c
ftp.wipo.int/pub/published_pct_sequences
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Sequence 996 BP; 366 A; 119 C; 202 G; 309 T; 0 U; 0 Other;

Local Similarity 635 AAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCA 694 Conservative 49.6%; 0, Score 170.6; DB 7; Pred. No. 4.9e-18; Mismatches 469; Indels Length 996; 6

755 TACCGAAAAATTTAAAATTATTTACCCACATATCATCTACCAGACAACATATATGCAACC 814 AGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACA 874 CÁCCATCAÁAATAAACGTTÁTTTAAAAGATGTCGTTTTÄGATAGTAGAATTTAAAGCAACT 186

GCÁATGCGCGAAGTTÁCÁAGTGAÁATTGATAGTTTAÁTTGÁTTCTÁAGAAAÁCTTTTATT CAACAATTACGCACCATATGTACACAAATACAACACAAACAGCATATGTGTAAAAATACT 934

935 CCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATA 994 CATGTTGCÁAAAGGTÁTAGÁAAATGATACÁTTCÁAÁCGTGTTTCÁGAAATGÁTTGAAGAT 366

1055 GAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGGT 1114

1115 GAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATT 1174 GAAGTAGTGATTAAACAACCAACTACAGTCGCCGCATCATCAAAAGATGAAAAAGTTAGT

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ACF75135 ID ACF75
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                        The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                    New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                    Claim 6; SEQ ID NO 5629; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus DNA #2815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACF75135 standard; DNA; 996 BP
       the novel S. aureus genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2001; 2001GB-00007661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2002; 2002WO-IB002637
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                                                                                                                                                                       1526 AATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTA 1585
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                                                                                                                                                                                                                                           832 AATATGGTTGAAGGTATTTATACAACTAAATCAGTTTATCATTTAGCTAAAGAAAAA
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                                                                                                          AATGTGGATATGCCAATTACAAATGCATTATATAGAGTATTÄTTTGAAAATATCTCAGTA
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       51.4%;
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Pred. No. 1e
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1e-17;
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                                                                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential to C prokaryotic cellular proliferation, their use in identifying the genes, and the use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia C coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also cuseful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent cd did not form part of the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                       Matches 505;
                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-025825P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
                                                                                                                                                                             Sequence 999 BP; 347 A; 134 C; 210 G; 308 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 8974; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; ds; prokaryotic cellular proliferation gene; antibiotic, antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus DNA for cellular proliferation protein #1649.
                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
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                                             635 AAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCA 694
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AAAATTACCGTTTTTGGTATGGGAAGTTTTGGGACAGCCCTTGCCAATGTTCTTGCAGAA
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                                                                                       Conservative
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                                                                                                             Score 168.6; DB 4;
Pred. No. 1e-17;
                                                                                Mismatches
                                                                                     454;
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                                                                                                                                Length 999;
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  19-JUN-2003
                                          ACA27525;
                                                                                       ACA27525 standard;
                                                                                                                                                                                                                                             1586 GATAAAGCCATATCAAACATATT 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1406 ATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAAC 1465
                                                                                                                                                                                                                                                                                                                                                                                                                      1466 CTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTT 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1346 ATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAAT 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1286 ATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTA 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1226 GGAATAATCGCTGGAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAACTAAAGGC 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1106 GAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCAT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418
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                                                                                                                                                                                                                                                                                                                                                                              832 AATATGGTTGTTGAAGGTATTTATACAACTAAATCAGTTTATCATTTAGCTAAAGAAAAA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 CTAGGTTTAGGTGGTATCGGTGACTTAATCGTTACTTGCACATCAACACATTCTCGGAAT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 658 TTAGCGGAAATTAGTAGA-----TTAGGTGAAAAGTTAGGTGCCGATCCTATGACATTT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 GATGACTTGATTGGTGTTGAACTTGGTGGTGCATTGAAAAATATCATCGCAGTAGCAAGT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 ATTGAAGATTCTATTTCACCTGAATATAATGCAGGTATTGGCGTGTTGTCAGGGCCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 AÄÄGCÄATGĆGAGAAGTTGCTTĊTĊÄÄÄTTAÄTGÄTÄÄGĊ-----TGACCTCTÄÄAÄÄG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       875 CAACAATTACGCACCATATGTACACAAATACAACACAAAAAAATATATGTGTAAAAAATACT 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 TCAGATATGACCAAAGCAATTCAATTTGCAGATATTTACTTAATGG---CTTTTACCTACT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               815 AGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACA 874
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                                                                                                                                                                                                                                                                                      AATGTGGATATGCCAATTACAAATGCATTATATAGAGTATTATTTGAAAATATCTCAGTA 951
                                                                                                                                                                                                                                                                                                                                AATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGAAGAATTTT-----ACAATATAATCCAATTTTTATACTCTCTGGTCCAAGT 1045
                                                                                                                                                                                                  AAAGAATGCGTAAAAGATTTAAT 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCACATTAGGATATAAACTTGGACAAGGTGAATCAATGGATCAAGCATTATCTGAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGCGGAAGAAGTTGTAGTCAAGCAACCAACTACAGTTGCTGCTTCATCAAAAAGATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATA 994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTATCGTAGCTGGAATTGGCTACGGTGATAATGCAAAAGCTGCATTAATGACTCGTGGC
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  (first
                                                                                       DNA; 999 BP
  entry)
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297

Prokaryotic essential gene #9182

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CC the 6213 antisenses esquences given in the specification where expression CC (1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid concoling a polypeptide whose expression is inhibited by the antisense cC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC antisense nucleic acid; (4) an antibody capable of specifically binding CC polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway for a gene product or that has an activity against a biological pathway or a gene on which the test compound that influences the biological compound; a activity; (11) a culture compising strains in which the proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an CC compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of Strains; or (13) identifying the target of a compound that inhibits the extent compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational content of the proliferation to isolate candidate molecules for rational content discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, CC prokaryotic essential genes. Note: The sequence data for this patent did content of the printed specification, but was obtained in the target prokaryotic essential genes. Note: The sequence data for this patent did cells only in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001Us-00948993.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
7-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; SEQ ID NO 15395; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug design;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; ds; prokaryotic
Sequence 999 BP; 366 A; 123 C; 236 G; 274 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELITRA PHARM INC.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                essential gene; cell proliferation;
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Forsyth RA,
  0 Other;
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Xu HH;
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1188
                                                                                  1548 TATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAG 1592
                                                                                                                                                                                                                                                                  1488 GTACTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCA 1547
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905 CTTCACTTTATAAGGTTCTATTTGAGAATGGAGATCCTAAAAAAG 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   611 ATGGTGACAACACAAAAGCGGCGCTTATGACAAGAGGTATGAGTGAAATAATGAGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        768 TAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAGACG 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       708 TTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAAAATT 767
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                                                                                                                                                                                    <u>AAGCGTGTCÁCACCTTTTATGAATTÁAAÁGÁATCCTTAGGTGTATCTATGCCAATTACCA</u>
                                                                                                                                                                                                                                                                                                                                                                    ĠTAGGĠGGATGTCATGTAGGGAAGCATGTGATAAAATAGGAATGGTAGTAGAAGGCGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGAAGGAACCA 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTTATAGTTACATGTACTAGTATGCACAGTAGAAATAGAAAGGCTGGTATACTAATAG 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGGAGGAGCAGTTAAAAATATAATTGCTCTAGCATCTGGAATAGGTGATGGAATAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGA 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATATTCCAACTACAGTAGTGGTTACTTCCACAGATATGAAATATGCAGAAGAAGTTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCAAAAGGCATGGAAGAAGAGACCAAGAAGAGGCTGTCTGAAGTAGTTAAAGAAGAAC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGG---CAGCTAAGGAAAGCAAATATATTGTTCTTGCTGTCCCATCTTTTGCTATAAGGG 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ATAGGCGTAAAGCTTGGAGGTAAGCCAGAAACTTTTTTTGGACTTACAGGCATGGGTG
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Matches

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Mismatches

Indels Length 999;

15;

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Local Similarity

3.5%;

Score 168.2; DB 7 Pred. No. 1.2e-17;

DB 7; 448;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 157-671; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention therapy of infections, particularly Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C, White OR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 910715 BP; 327171A; 129646C; 130753G; 323091T; 0U; 540ther;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-081217/07
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Similarity 49.4%;
TTTTTTTACAGATGCTATTCATAAAATACCTACAAATTCCGGTATATCTGTACAATATT
                                                                                              ÄATÖGTÄATÄATAGÄGAĞCTTTCATTĞCATCÄTTAGAAAGAGTTTTTTCTTCTCTATTGT 105962
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                                                                                                                                                         ATTCATATGACTGCATTGCTATTAAAGCTTCATCACTTAATACATGAGTACACAAACCTA 2840
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                                                                                                                                                                                      3840 AAATATACAAT 3850
                                                                                                                                                                                                                                                                                                         3780 TTAATATATCTTTTATTAGATTTCTGATATCAACTTCATCAACAACTAATACTTCAG 3839
                                                                                                                                                                                                                                                                                                                                                                                                                              3720 AAGCCATCTTGATCGCGGATAAACCATCAACTGCTAATTTAGTGACATAATTATCATCAC 3779
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                                                                                                                                                                                                                                                                                                                                                                          CAATTGTTTCAAGAGCTTCTTCTCCGTCACTAGCAGTGAAAAACAAAATATCCTTCATCCT 105014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGATATCTGGGGCATTCT-----CAGGTCAGATATTATTACATCAAGATTTTCATTTT 10507
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Best Local :
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Sequence split into
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                                                                                                                                                                                                                                                                                                                  3201 TTTCCTCACTACCAAATATATTAACCAAGTAATTATTAGCTGGTAGCATAGATGAGTACA 3260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598;
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                                     AT-GCTGATTTCAACTCATCATTTTCTCTACGTAATCTACCAGA------ 3483
                                                                                                                                                                                                                                           TAGATATAAATGGAGTATCATACCCCTTGGATTTTTTATGTATTAGCCTAGCAACTACTT 3320
                                                                                                                                                                                                                                                                                                                                                     TGTTTGCAAGTTCAAATCTGCCTTTTTTTTTTGGAAATTGCTCCAGTGAATGCT-----C 5608
                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGCTTGACTTGAATTTCAGGTGAAATTTCTGCTATCTCATCAAGAAAAATTGTGCCTT
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TTAGATCTTTTCTTATTAGTATATTTTCTAAATTAGCATTTTCATTATCGTTATTTTCTT 5308
                                                                     TTACAAGTTCAAAATTTTTTTGCATTAATAGGGATTTTCCCCATGATTTTTTCATAGTATT 5368
                                                                                                        TAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTATTTCATAATCCTCAA 3440
                                                                                                                                        CTTTACCAACACCGCTTCGCCCGTTATAAGAATAGATGCATTTGATTTTGCTATTTTTA 5428
                                                                                                                                                                        CTTTTTCATGGCCAAAAAGTTCACTTTCAAGAATGCTTTCAGAAAGTGCTGCGCAATTTA
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10 fragments LOC
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Pred. No. 3.4e-17;
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                                                                                                                                                                                                                                                                                                                                                                          Wang L,
Wall D,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                         Claim 14; SEQ ID NO 34158; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prokaryotic essential gene #27945
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DB; ABU42418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                          Zamudio C,
Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                              Zyskind JW;
Xu HH;
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The invention relates to an isolated nucleic acid comprising any one the 6213 antisense sequences given in the specification where express

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of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
cencoding a polypeptide whose expression is inhibited by the antisense
concluded acid; (2) a host cell containing the vector; (3) an isolated
containing the polypeptide; (6) inhibited by the
containing the polypeptide; (6) inhibited by the
containing the polypeptide; (6) inhibited by the
containing the polypeptide; (6) inhibiting cellular
containing the polypeptide; (6) inhibiting cellular
containing the gene in an operon required for
containing a gene activity of a gene in an operon required for
containing a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
containing proteins or screening for homologous nucleic acids are useful for
containing proteins or screening for homologous nucleic acids required
containing the target of a compound that inhibits the
containing proteins or screening for homologous nucleic acids required
containing to proliferation to isolate candidate molecules for rational
containing the proliferation to screening homologous nucleic acids
containing to proliferation and cells other than S. aureus, S. typhimurium,
containing the proliferation for screening homologous proless acids required
containing the proliferation to isolate candidate molecules for rational
containing the proliferation to isolate candidate molecules for this patent did
containing the prolifer
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
1166 CAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGT
                                                                                                                                                                                                                 1106 GAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATATACCAT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                         1046 TTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAA 1105
                                                                                                              478 AGTGTAAGTAAATTAACGCAAGATTTATTTATGAATGATTATTTGCGTGTGTACACGAAT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 ATTGAAGATTCTATTTCACCCGAATATAATGCAGGTATTGGCGTGTTGTCAGGGCCAAGT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695 CATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 AAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503;
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                                                                                                                                                                                                                                                                                                                                CATGCGGAAGAAGTTGTAGTCAAGCAACCAACTACAGTTGCTGCATCATCAAAAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGAAGAAATTTT-----ACAATATAATCCAATTTTTATACTCTGGTCCAAGT 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTITIATACATGITGCTAAAGGTATTGAAAATGGGACGITTAAACGTGIGICAGAAATG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCARTATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATA 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGCAATGCGAGAAGTTGCTACTCAAATTAATGATAAGC-----TGACCTCTAAAAAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACAATTACGCACCATATGTACACAAATACAACACAAAACAGCATATGTGTAAAAATACT 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGATATGACCAAAGCAATTCAATTTGCAGATATTTACTTAATGG----CTTTACCTACT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACA 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCATACAAATAAAAAGTATTTAAAAATACGCGAAAATTAGATGTTAACATCATCGCTACT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCGAAAAATTTAAAATTTTACCCACATATCATCTACCAGACAACATATATGCAACC 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGGACATGATGTTTTGATGTGGGGGTAAAAATCAAGATGCTGTTGATGAATTAAATACA
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative of

disorders

Claim 28; SEQ ID NO 386; 117pp; English.

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent tidistinguishes between methylated and non-methylated CpG dinucleotides.

a reagent that

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CCCXBXFFFEXRXFITTTFFFXBXRXFXBXAX
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                                                                                                                                                                                                            Berlin K, Braun A, Distler J, Guetig D, Howe A, Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesc Lewin A, Lipscher E, Maier S, Model F, Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haematopoietic cell proliferation disorder related DNA sequence #386.
                                                                                                                                                            WPI; 2003-018942/01.
                                                                                                                                                                                                                                                                                                                       26-MAR-2001; 2001US-0278333P.
                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002; 2002WO-EP003401.
                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytosine methylation state; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ10246 standard; DNA; 8056 BP
                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1526 AATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1466 CTAAAGCTTGTTGAAGGAACCAGTACTGTAAAAACCACTGATATCATTAGCAAAAAAACTT 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1346 ATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAAT 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1226 GGAATAATCGCTGGAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAACTAAAGGC 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               832 AATATGGTTGTTGAAGGTATTTATACAACTAAATCAGTTTATCATTTAGCTAAAGAAAAA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 TTCACATTAGGÁTATAAAACTTGGÁCAAGGTGAATCAATGGATCAAGCATTATCTGAAATG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        712 CTAGGTTTAGGTGGTATCGGTGACTTAATCGTTACTTGCATATCAACACATTCTCGAAAT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598 GGTATCGTAGCTGGAATTGGCTACGGTGATAATGCAAAAAGCTGCGTTAATGACTCGTGGT 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           538 GATGACTTGATTGGTGTTGAACTTGGTGGTGCATTGAAAAATATCATCGCAGTAGCAAGT 597
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                                                                                                                                                                                             Lipscher E,
, Ziebarth H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
830 GTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACAACAATACGCACC 889
                                                              770 AAATATTTACCCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAGACGAA 829
                                                                                                                                           710 AACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAAATTTA 769
                                                                                                                                                                                                                             650 GGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTT
                                                                                                                                                                                                                                                                                                             590 ATATAATTTTTTGACTGGTTTCTTGATTATAAATTAGGTAAAAAATGAAAATCAGTATTTTA 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 ACTTATTAATATTTCAAATTTATTATTACTACTCATCA--TATTTAGCATAATATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 TAGAGTTCTTTATTCGACATACATATTAAAATCAATCAAAACAAAATAATAGTACTATCT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 GTATTCAAAGAATACCTCTTCTCTTGTTCCATCCATATTTTCCAATTATTTACAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 AACCATTITCTCAAATCTCCAATTTTAACATGCACAAGATTATTTAATGTAACAGAACAC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 CCTGTACTCTTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAACT 291
                                                                                                                                                                                                                                                                                                                                                                                             AATTAATAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAGACACTTA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 1393; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 162.2; DB 7; Length 8056;
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                                                                                                                       1843 ATAAGTCAAA-----TTAAACTTTTACTTATTTATAAAATAATATGTTTTGCACACTTTT 1896
                                          1897 TCACTACATCATGTATATAATGAACATAATTTTACATAAAATAACTAATAAAAAAGAACCA 1956
                                                                                                                                                                 1310 ATAGCAAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCATCATGTCTTGGAGAT 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1130 ACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGATT 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         937 -TTTTTAAAAATTAAATTTTTATTTTATTTAAATGAATAAAATATATATATATTAATTTT 995
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                                                                                 ТААПТАПАЛААСАААТТССТАТСТССТАТСТСААТТААССААТТGTTATCAGATTATAA 1842
                                                                                                                                                                                                                                                                                         AAGTATGTAACATATTACATAACA-----AACTTAAGTATAACTTAAAATTTCCTAGC 1782
                                                                                                                                                                                                                                                                                                                                 GAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACT 1729
                                                                                                                                                                                                                                                                                                                                                                                                                   TCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTA 1609
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                                                                                                                                                                                                                                               AAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGT
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                                                                                                                                                                                              DNA encoding Acinetobacter baumannii protein #3206.
                                                                                                                                                                                                                                                                                                                    ADA31919 standard; DNA; 1557 BP
                     13-MAY-2003
                                                                                                  Acinetobacter baumannii
                                                                                                                                                                                                                                       20-NOV-2003
                                                                                                                                                                                                                                                                                ADA31919
                                                            US6562958-B1
                                                                                                                                         vaccine; plant biocontrol agent
                                                                                                                                                          gene; Acinetobacter baumannii; bacterial disease; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2668 CGAATTAGATACTATATCTACTGGTAAATCTTTTGCTGTAATCATCT 2714
                                                                                                                                                                                                                                                                                                                                                                                                                     TAAATAAATTATTAATAAAAAATAAAAATATTTAATTGTTTATTT 2777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCACGAGCTTTACGTAATGGTACAGAAATAACTTTAGCACTTAAAAACATCATTAATAGG 2667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTTCACAATTCATACATAAATAATTATACATGCAATGTTTATTCAGAAACATTACACAA 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTAATTTTTGTATTTAAATAAATTTTAATTTTÄAATATÄAATTTTTÄTÄTTTTTA 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTATATTTATACAATTACAAAAT 2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ТАТАЛАТААТТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАТСТТАЛАЛТТТАЛАЛТТТАЛАЛАТА 2672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGTGATACATTACCTCCAAAACGAGATAACTGAGTTTTTTAAATACTGTCTTTCAAATTC 2601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTTTATGCCCATTAGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAATACA 2130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of a baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1557 BP; 481 A; 321 C; 330 G; 425 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; SEQ ID NO 3206; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ADA36045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                      3239 GCTGGTAGCATAGATGAGTACATAGATATAAATGGAGTATCATACCCCTTGGATTTTTTA 3298
                                                                                                                   3179 CTATGAGACAATATATTATTACTTTCCTCACTACCAAATATATTAACCAAGTAATTATTA 3238
                                                                                                                                                                                                3119 TCATCTATAAATAACGTACCATGATTTGCTTGCTCTATAATTCCAATATGAGGAGGTACT 3178
                                                                                                                                                                                                                                                                                                                                                           2999 GAAGACAATAATTCTCACATCTATACTAACAGGAATCTTACTATTTTCCCTATATATT 3058
                                                                                                                                                                                                                                                                                                                                                                                                                                        2939 CTATAATATAAATCCTCACAAAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAA 2998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1028 ATCGGGÄTGTCTTCACTGCGATGCGCAÄGCTTCGGAATATGAATTCGAATAACATTTAGA 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2699 TTTGCTGTAATCATCTCCTTAGGAGATTTCATAATTAAAATCCATTCTATAACATTACGT 2758
674 TTAGGAATTGCTGCCATGTTTÄAÄGCAATAAAAGGCTTAGCGCGTCGTGGTGAATGTTTA
                                                                               728 GCACCCGTGAA--
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                                                                                                                                                                                                                                                                           TTTCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTATCGTATCGTAAATCTGTTACT 3118
                                                                                                                                                                                                                                                                                                                    GTTGCCGCGACAATTCTGACATCTTATACGGGTATATGTCCACCAACTCGGTAAAAC 849
                                                                                                                                                                                                                                                                                                                                                                                               CGGTGGTATAAGTCTTCACGGAAACGACCTTCATTCACCAGTTTTTCTAAGTCTTGATGG 909
                                                                                                                                                          TCATCAAGGAATAGTGTTCCGCCATTTGCTTGTTCAAAGCGGCCTTGATGTTTGGGTGTTT
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48.3%; Pred. No. 2.4e-16;
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       WPI; 2002-500450/53.
                                                                                                                                                                                                         06-DEC-2000; 2000DE-01061338
                                                                                                                                                                                                                                                                     06-DEC-2001; 2001WO-EP014320.
                                                                                                                                                                                                                                                                                                                                                                                                        WO200246454-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human angiogenesis associated polynucleotide SEQ ID NO 123.
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                                                                                                                                         (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis or treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44631 АССАЛАЛТТСТАЛАЛАЛАТТАСЛАЛСАЛАЛАЛАЛАЛАЛАТАЛАЛТТАССАТСТТТТТТАЛ 44572
                                                                   864 CTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAACAGCATATGT 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       630 AAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGT 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 3.4%; Score 159.6; DB 6; Length 83391; Similarity 44.3%; Pred. No. 3.2e-16;
          CATTTACTACATATCAATAA--AAATACCATTCGCTAAATCAAACACATAAAAAATTAAA 44214
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 1239; Indels
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New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in

bases of chemically pretreated DNA of angiogenesis-associated genes (I) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences The invention relates to a nucleic acid (I) comprising a segment of 18

Sequence 83391 BP; 25113 A; 665 C; 16761 G; 40835 T; 0 U; 17 Other;

44931 ATTACGTTATTTAAAATATTAAATACTCAAACCAACCGAAACACAAACCAAAATAAAAAA 44872 210 ATTATTTAATGTAACAGAACACCCTGTACTCTTATGCAAGAACTCTATAAACTTATCAAG 269 17; Gaps 80

44871 TTTAAATAAAAAAACATATAAAAAAAAACTACTAATAAATACAAAACTCAATTAAATA 44812

44811 TAAATAATTATAAATTAATTATCTTTTTÄTTTAAAAATCTAATAAATTCTAATTT 44752

390 AAACAAAATAATAGTACTATCTAATTAATAAAAAATCCTCAATAGTCTTTAGCAAGAAC 449

44691 AÁACTÁAAAACTCCGAAAATTCCTCAATAATATATACCAAAAAACAAAAAATTTTCCACTA 44632

510 ATATTTAGCATAATATCACATCTGACATGATTAACAATAGTAACACATTTCTTAACACTA 569

GATAATATACAATAAATATATATAATTTTTGACTGGTTTCTTGATATAAATTAGGTAAA 629

AAAAAAAAACTAACCCCAATTTAACTTCTAAAATAATAAAAACCATTTTAACCACACTTT 44452

44451 CCCTAATATTAATTACTATTTTCTTACACTAACTTAAAACTACAATTACCCATAAAATAT 44392 CAGCACATGGTATATCAGTTAACTTATGGGGGACGTGATCATAGAAATATTACACATATAA 749

810 CAACCA----GCAATATAGACGAAGTATTATCTGACAAC--AATACATGTATTATCTTAA 863 ACACTTACCGAAAAAATTTAAAATTTTACCCACATATCATCTACCAGACAACATATATG 809

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44033 AĀĀĀĀĀĀĀĀĀĀĀĀTĀTĀTĀCĊĀĀCĀĀŤTĀTĀTĀĀĀĀŤĀĀCCĀĀĀĀĀĀĀĀCĀĀĀĀŤTĀĀĀĀĀĀCĀTĀ 43974
                     43258 CAATAATAAAAAAAAATTCTACCAACCATCCAAAAAAATAAACATTTTACCTATAAAAA 43199
                                                                                                                                                                                                                                                                                                                        43378 САТРАСССБАРАЛАЛАЛТТССТТРАТРАРТАЛАТАЛАЛТЕРАЛАТСТАСТТАСАСТАРАСТАРА 43319
                                                                                                                                                                                                                                                                                                                                                                                                                          43438 АЛАЛАТЛАЛАТТССТАЛАСЛАЛАЛАЛСТАЛССЛАТТТАЛАСЛАЛАЛАТЛАТТЛАЛАЛ 43379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43558 АЛЛАТСGЛАТСЛАСАТСЛАЛАЛСАЛАЛАТЛАЛАТТАСЛАЛАЛАЛСЛАДТТАЛАЛАЙТАЛАЙЛАЙ 43499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43734 ATATAATAATTTTTAAACTTTAAA----AACTATTCATAACATAAACACTATAAAACAATT 43679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43794 ААСАААТАЛАТСТІТАТІТАЛІТТАТІТАТТАТАТАСАДАТАЛАТССАЛЛАТАЛАТТАЛАЛА 43735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43854 АЛАРАРАРАРАЛАЛАСАТРАТАСТСРРИЛАЛАЛАЛАРАРАРАСТТТТЕЛАЛАЛАЛАЛАТТТАТ 43795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43914 AAAATAAATAAATAAAAAAAAAAAAATTAAATAACAATAAATTATAAAATAACGTATTÄT 43855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1642 CAATGATAAATAAACGGTCAAAAATATAGAATACAACGTTCACCACATATATAAAAAGCA 1701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1402 CAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCA 1461
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                                                                1881 ATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACATAATTTTACATAAAATAA 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1702 GTCAAATACCCCATCGTTAACATCCAACTAAGTATGTAACATATTACATAACAAACTTAAG 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1582 ACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTCAACA 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1522 ACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATC 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1282 AGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATAC 1341
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                                                                                                                                                                                                                       ATCAATATACGTAAAAAAAAAATACATATCCAAAAATATTCTAATATTTTTCTTATTT 4325
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                                                                Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                   15-MAR-2000; 2000DE-01013847

06-APR-2000; 2000DE-01019058

07-APR-2000; 2000DE-01019173

30-JUN-2000; 2000DE-01032529

01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
                  Claim 1; SEQ ID NO 252; 27pp; English.
                                                                                                                                                                       WPI; 2001-602752/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2001; 2001WO-EP002955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour suppressor gene derived chemically modified sequence #252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS46530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS46530 standard; DNA; 7814 BP
                                                                                                                                                                                                                     Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2420 AAAAGATGACTTCACAATTCATACATAAATAATTAT 2455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2300 АЛТТАСАААЛТТТССААСТТСААСААСАААЛСАААСТСАААСТСТАТТАТАСАААТТСААСА 2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2241 TAAGA-TATCCCTACAGCATGTATCAAATAATAAAGAAAATCGTTATGTATATTTATAC 2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2181 СЪРАТТТСТЪАТАТЪРССТАСССТЪСТСТЪРЪССТЪСБЕВЪССЪРТТАСТАТСТЪР 2240
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CC The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CP blaulphite, of genes associated with tumour suppression and oncogenes CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and C500 are missing from the sequence listing) sequences (SS) and sequences (CC complementary to (SS). The nucleic acid may be a peptide nucleic acid—CC probes for detecting the cyrosine methylation state and/or single—CC nucleotide polymorphisms and also to be used in an array for analysing CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or cpjgenetic parameters for the diagnosis and/or therapy of existing CC diseases or the predisposition to specific diseases, by analysing CC diseases or the predisposition to specific diseases, by analysing CC genetic and/or epigenetic parameters may be compared to another set of genetic and/or prognosis events which are disadvantageous to CC cyrosine methylations. The parameters may be compared to another set of genetic and/or prognosis events which are disadvantageous to CC partents. The present sequence is one of the S3 genomic sequences can incorrect Seq ID numbers are the complementary sequence of the CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID CS 135, except for those whose partner sequence is missing). Note: The S9 sequence data for this patent did not form part of the printed CC sequence data for this patent did not form part of the printed CC sequence data for this patent did not form part of the printed CC sequence at the complementary sequence of the S9 sequence at the printed CC sequence at the printed S9 sequence at the p
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Best Local Similarity
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                                                                                                              5341 ATAACACACACGAATAAATAAATAAACACATCAAACAAAACCTAAATCTTATAAAATAAA 5282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5401 AAAAAAATAATTAAATAAATAAATAAATAAATAAACATATAAACAAACCAAAACAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5461 TTCTCCATTATACAATATATCCATAAAACAAAACTACATTTATACCCCCTTACATTTATAC
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                                                                                                                                                                                                                                                                                                                                                                                                      968 ACATCACTCAAATTTCCCAGTGAAATAGCAGAAAGAAATTTTACAATATAATCCAATTTTT 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671 GCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCAT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611 TTGATATAAATTAGGTAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491 ATTTATTATACTACTCATCATATTTAGCATAATATCACATCTGACATGATTAACAATAGT 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 AACACATTTCTTAACACTAGATAATATACAATAATAATATATAATTTTTTGACTGGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACAAACAGCATATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATT 967
                                                                                                                                                                                                                                                            TTRATCAAATTCCTAAAAACCCTAAAAACCTATAACCTAAAACCTTTAAAAATCCCAA
                                                                                                                                                                                                                                                                                                                                 TGTATTA----TCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAA 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
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   1981 ACCTATTTACTACGTAATATTACATAGATGTCCTGACAT-AATAAATTCTATCATCCTTG 2039
                                                                                                                                                                                                                                                                                                                                                                                                                                    4144 АЛААЛАЛАТЛАЛАТТАТАТСТТТАСЛАСАЛСАТАЛАПЛАЛАТТАЛАЛАЛАСАТТАТСАТА 4085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1868 TITATAAAATAATATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACATAATT 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1688 ATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATTAC 1747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4324 TAÄATAÄÄTÄÄCTÄÄATÄÄÄTÄAATÄATACCAÄAÄAAATÄCTACATTTATATATTTATCA 4265
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                                                                                                                                                 TACGAAACAACGCAAAAACAAAAATCAAATACTACCTATTCTCATAAAACTCCTAAAAA
                                                                                                                                                                                                                                                                                                                                                            ТТАСАТАААТААСТААТАААААСААССААТАС-----АТАТАТТАААТТАСТААААС 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTATCTCAATTAACCAATTGTTATCAGATTATAAATTAAGTCAAATTAAACTTTTACTTA 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAACACTATTCATAATAACAAAAATACAAAATCAACATAAATATCCATCAACGAATAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACAAATTCCTATCT 1807
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                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                            Prokaryotic essential gene #15557
                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACA33900 standard; DNA; 1065 BP
                                     Claim 14; SEQ ID NO 21770; 1766pp; English.
                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                          21-MAR-2001; 2001US-00815242.
01-18-2001; 2001US-00948993.
25-0CT-2001; 2001US-00342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                03-OCT-2002
                                                                                                               P-PSDB; ABU30030.
                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107.
                                                              isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
invention relates to an isolated nucleic acid comprising any one of 6213 antisense sequences given in the specification where expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2160 ATACACGTCAAATAAATTAAACAAATTTCTAATATAACCACCTACTCTAAAACATAGGAAC 2219
                                                                                                                           2003-029926/02.
                                                                                                                                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTA 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCTATTATAACAAATTCAAGAATTATATATACTTCACCAACACATAGTTATCAAATTC 2396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATAGTATATCATACCTAAGTAAGATATCCCTACAGCATGTATCAAATAATAAGAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAACAATATGAAGAAGATACA 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                              Malone
                                                                                                                                                  Malone C,
Carr GJ,
                                                                                                                                                            Haselbeck R,
                                                                                                                                                  Yamamoto R,
                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                                                                                  Zyskind JW;
Xu HH;
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of the nucleic acid inhibits proliferation of a cell. Also included are:

(C (1) a vector comprising a promoter operably linked to the nucleic acid
ce encoding a polypeptide whose expression is inhibited by the antisense
culsic acid; (2) a host cell containing the vector; (3) an isolated
cpolypeptide or its fragment whose expression is inhibited by the
cardi; (4) an antibody capable of specifically binding
ct proliferation or the activity of agne in an operon required for
cproliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
cy required for proliferation, or that inhibits cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
cy a gene on which the test compound that inhibits proliferation of an
compound's activity; (11) a culture comprising strains in which the gene
cy roduct is overexpressed or underexpressed; (2) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
cy roduct is overexpressed or underexpressed; (2) determining the extent
cy for cellular proliferation in cells of a compound that inhibits the
cy roliferation of an organism. The antisense nucleic acids are useful for
cy identifying proteins or screening for homologous nucleic acids are useful for
cy collilar proliferation in cells other than S. aureus, S. typhimurium,
cy proliferation for life streetly from WIPO at
cy sequence 1065 BP; 358 A; 172 C; 248 G; 287 T; 0 U; 0 Other;
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SQ Sequence 1065 BP; 358 A; 172 C; 248 G; 287 T; 0 U; 0 Other;

Query Match

3.3*; Score 155; DB 7; Length 1065;

Best Local Similarity 49.0*; Pred. No. 1.4e-15;

Matches 504; Conservative 0; Mismatches 515; Indels 10; Gaps 3;

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                                                        1062 CAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCAT 1121
                                                                                                                                                          1002 AAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTG 1061
                                                                                                              427 GAA--GAAAAAAGACAGGCAATTGTTGTATTATCTGGTCCTAGCCATGCTGAGGAAGTGG
                                                                                                                                                                                                                            367 AAAGGACTAGAACAAGATACGCÁTAAÁCGAATCTCAGAAGTTTTGGCTGÁÁGAAATTCCA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 GATGTCCGTATTTGGGGAAATGTACCTGAACAGATTGATGAAATCAATAAGTATCATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 AATAATATATATTTTTGACTGGTTTCTTGATATAAATTAGGTAAAAAATGAAAATCAGT 643
                                                                                                                                                                                                                                                                                 942 TAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAATAGCAGAAG 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 TCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         644 ATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 GTTCTTGGTCCTGGATCTTGGGGCACTGCTTTAGCACAAACATTGGCAGAAAACGGGCAT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTATAATGGAAATTATCAATTATTTATTTGGAGGAATATCCATGAAACAAAAATCGCA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCAGCATTTTTACCTGATTTGACGATCCCAGAATCGATTATCGGATATAAAGAATTG: 246
                                                                                                                                                                                                                                                                                                                                                                                            TACGCACCATATGTACACAAAAACACACAAACAGCATATGTGTAAAAATACTCCAATAT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGAAGCAGTGGATAACGCAGATGCTATTTTÄTTTGTTGTTCCAACAAAAGCGATTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGAAGTATTATCTGACAACAATAC--ATGTATTATCTTAACTATTCCTACACAACAAT 881
  CAGTACATGATATCACAACAATTACAGCTGCAAGTATTGATCAAAAAGCAGCAGCCTATG
                                                                                                                                                                                                                                                                                                                                    TCAGTCGCACAGGAACTTATTGGTAAAATGAATACTAAGCCAATCATTATACATGCAAGT 366
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1122 TGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTG 1181

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Example 1; SEQ ID NO 350; 243pp; English
                                New isolated nucleic acid derived from Enterococcus faecium encoding .
Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                             02-JUL-1997;
14-MAY-1998;
                                                                                                                 Doucette-Stamm LA,
                                                                                                                                                                                               30-JUN-1998;
                                                                                                                                                                                                                                              US6583275-B1
                                                                                                                                                                                                                                                                   Enterococcus faecium.
                                                                                                                                                                                                                                                                                                    ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;
                                                                                                                                                                                                                                                                                                                           E. faecium DNA sequence SEQ ID 350.
                                                                                                                                                                                                                                                                                                                                                    01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                ADC90723 standard; DNA; 1071 BP
                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                          abdominal-pelvic infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1302 CACTATATATAGCAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCATCATGTC 1361
                                                                                2003-799836/75.
)B; ADC94377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             779 TGGGGGACTTGATCGTTACTTGTACAAGTGTTCATTCTCGCAATTGGCGTGCCGGTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 TAGAAACTGGTGCAGCACTGAAAAATATCATTGCAATTGGTGCCGGCGCCTATCCATGGAT 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 TACAAAAACTGTTCATGAATGATTATTTCAGGATTTATACAAATAATGATGTGATTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTACTCAAACAATCTATAATGTTTTGTATAATGGAGAGATATCAAAAAAGCAGCAAAAG 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTTGGTGTCGCGATGGGT-----GCCAATCCTCTGACATTTATCGGTTTGAGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGGATTCGGAGATGATGCAAAAGCAGCAATCATGACTCGAGGATTGGCAGAAATCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAGCCATATCAA 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTGGCAACGACAAAAGCAGCAGCAGAGAGCTAGCTCAACAGCTAGGTGTTGAGATGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTAGGACAGGGACATAAGCTGGAAGAAGTTCTAGAAAACATGGGAATGGTCGTTGAGG
                                                                                                                                                                           97US-0051571P
                                                                                                                                                             98US-0085598P
                                                                                                                                                                                                98US-00107532.
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                                                                                                                                                                                    430
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                                                                                                                                                                                                                                                                               310
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                                                                                                                                                                                    GAA--GAAAAAAGACAGGCAATTGTTGTATTATCTGGTCCTAGCCATGCTGAGGAAGTGG
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The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it. Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening decorations, wounds and abdominal-pelvic references and conditions and sequences and a sequences are consistent and actions are consistent and actions and actions are consistent and actions are sequenced.
infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represent one if the disclosed E. faecium nucleic acids.
                                                                                         The present sequence represents
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Sequence 1071 BP; 362 A; 172 C; 249 G; 288 T; 0 U; 0 Other;

Length 1071;

584 AATAATATATATTTTTTGACTGGTTTCTTGATATAATTAGGTAAAAAATGAAAATCAGT 644 ATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATA 703 504; Conservative GATGTCCGTATTTGGGGAAATGTACCTGAACAGATTGATGAAAATCAATAAGTATCATACA 189 ТСАGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAA 763 ACTATAATGGAAATTATCAATTATTTATTTGGAGGAATATCCATGAAACAAAAAATCGCA 69 GTTCTTGGTCCTGGATCTTGGGGGCACTGCTTTAGCACAAACATTGGCAGAAAACGGGCAT 129 3.3%; bu 49.0%; Pre Score 155; DB 9; Length 10 Pred. No. 1.4e-15; 0; Mismatches 515; Indels 10; Gaps

824 GACGAAGTATTATCTGACAACAATAC--ATGTATTATCTTAACTATTCCTACAACAACAAT 881 TCAGTCGCACAGGAÀCTTATTGGTÀÀAATGÀATÀCTÀAGCCAATCATTATÀCATGCÀAGT TACGCACCATATGTACACAAATACAACACAAACAGCATATGTGTAAAAAATACTCCAATAT AATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACCAGCAATATA 823 GCAGAAGCAGTGGATAACGCAGATGCTATTTTATTTGTTGTTCCAACAAAAGCGATTCGT AATCAGCATTTTTTACCTGATTTGACGATCCCAGAATCGATTATCGGATATAAAGAATTG 249 369

1002 AAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTTGCTAAAGAAATTG 1061 AAAGGACTAGAACAAGATACGCATAAACGAATCTCAGAAGTTTTTGGCTGAAGAAATTCCA 429 TAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATAGCAGAAG 1001

1182 TACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAA 1241 TACAAAAACTGTTCATGAATGATTATTTCAGGATTTATACAAATAATGATGTGATTGGCG 607 TGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTG 1181 TAGAAACTGGTGCAGCACTGAAAAATATCATTGCAATTGGTGCCGGCGCTATCCATGGAT 667

668 TÁGGATTCGGAGÁTGÁTGCAAAAGCAGCAATCÁTGÁCTCGÁGGATTGGCAGAAATCAGCC 727

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RESULT 22
ABL3336/c
ID ABL333
AC ABL
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiatteriosclerotic; antianaemic; cytostatic; nottropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarchritic; antidiabetic; antipsoriatic; antirheumatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL33396 standard; DNA; 5641 BP
                                                                                                                                                                Claim 1; SEQ ID NO 1369; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                      WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 1369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATCATGT 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTTAGGACAGGGACATAAGCTGGAAGAAGTTCTAGAAAACATGGGAATGGTCGTTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5641 BP; 1442 A; 34 C; 930 G; 3235 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4356
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                                                        TCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCATTGATAGAAAC 1131
                                                                                                                                                                   ATATAATCCAATTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAGAACATCT
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                                                                                                                TAPAGGTATCGAPATTACATCACTCAPATTTCCCAGTGAPATAGCAGAPAGAPATTTTACA 1011
                                                                                                                                                                                                                                                                                                                                         ATTAACAAAAATCAAACGAAACCTTCAAATTCTCCAATAAAAAATAAAAATAAAAATTAAA 4177
                                                                                                                                                                                                                                                                                                                                                                                         ATGTACACAATACAACACAAACAGCATATGTGTAAAAATACTCCAATATTAATTTGTAG
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Pred. No. 1.5e-15;
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ATGAAGAAGATACAATACACGTCAAATAAATTAAACAAATTTCTAATATAACCACCTACT 2205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAAATTAAACTTTTACTTATTTATAAAATAATATGTTTGCACACCTTTTTCACTACATCA 1907
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                                                                                                        TAGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAACAAT 2145
                                                                                                                                                                                                              TTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCAT 2085
                                                                                                                                                                                                                                                                     AAATAAAAAAAAACCAAATAAAAATCCTACAATCAAAATATACAATAACTAAAATAAAAA
                                                                                                                                                                                                                                                                                                                         AAATTACTAAAACACCTATTTACTACGTAATATTACA--TAGATGTCCTGACATAATAAA 2025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTAACAAATAAAACCTACATTATTCAAAAAATAACACATTAA-----AATAACT 3767
                                                 TTTTATTAATCAAACTAAATAATAATATTÄÄÄCTAACÄAÄÄÄAAAATAACATTCTTTAAAA 3051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTAAAACCACTGATATCATTAGCAAAAAACTTAATGTAGAACTACCAATTTGCATATC 1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATAATTAATTTCGAAAAACTAATTCGAACAATATTTTATATCTTATCAAACACATTTA 3707
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                                                                                                                                                                                                                                                                     3111
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CTCAAAAAAATATAAAACACCATTAAACATACCAACACACATAAAATACAAATACTAAAA

This sequence represents one of 5191 Staphylococcus aureus DNA of the invention. The DNA sequences are recorded on a computer medium, preferably selected from a floppy or hard disk, random

access sequences

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RESULT 23
AAV74824/c
ID AAV748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                  Claim 1; Page 1440-1441; 3271pp; English.
                                                                                        Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of \hat{\epsilon}
                                                                                                                                                                                                                                       07-JAN-1997;
                                                                              S.aureus vaccines.
                                                                                                                                WPI; 1997-374922/35.
                                                                                                                                                          Kunsch CA,
                                                                                                                                                                                                               05-JAN-1996;
                                                                                                                                                                                                                                                                  30-JUL-1997
                                                                                                                                                                                                                                                                                            EP786519-A2
                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus contig SEQ ID #513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV74824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV74824 standard; DNA; 918
                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2506 A 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2446 AAATAATTATACATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2690 AACAAACTTCTCAACAAAAACAAAAAAAAAACTCCAAAACAATTAAATAACATATTCAAAAT 2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2930 ААСААЛААААААЛАААТСАААААААЛАТССААДААААААДАТААСТАДАААССТТААТАА 2871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2206 CTAPACATAGGAACCAATAGTATATCATACCTAAGTAAGATATCCCTACAGCATGTATCA 2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATCAAATTCTATAATACATCATATCCTTTTTAAAAAGATGACTTCACAATTCATACAT 2445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ААТААТААДБААЛАТССТТАТСТАТАТТТАТАСААТТАСААДТТТССААСТТСААСА 2325
                                                                                                                                                         Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                               96US-0009861P
                                                                                                                                                                                                                                                                                                                                                                                                                             aureus
                                                                                                                                                                                                                                       97EP-00100117
                                                                                                                                                                                                                                                                                                                             /note= "these bases represent a line of missing text
the sequence listing in the specification. They are
included to maintain the nucleotide numbering given i
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                     . 840
                                                                                                                                                          Barash SC,
                                                                                                                                                         Dillon PJ, Fannon MR,
                                                                                                                                                          Rosen CA;
                                                                                           of anti-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The slaves in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer readable magaium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 918 BP; 271 A; 177 C; 113 G; 297 T; 0 U; 60 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the S.aureus DNA sequences allows putative functions to be assigned so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      memory (RAM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                 1622 ATCCTTTGATAATTTCAACACAATGATAAATAAACGGTCAAAAAT 1666
                                                                                                                                                    1562 TTATTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATC 1621
                                                                                                                                                                                                                                                    1502 CTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAAT 156
                                                                                                                                                                                                                                                                                                                                                         1442 ATAAATACATTAATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1382 TGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAAT 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1322 CATTCAATAGATCTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACA 138:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1202 AAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAAATTTAGGTAATAATGCT 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1142 GATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTA 120:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1082 ATAGTACTTGCTGGTGATAATAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAAT 1141
138 AAATCTGAATAAAATGTGTATTATTACACATATACGGCTAATAAT
                                                                                               198 GTATTATTTGAAAATATCTCAGTAAAAGAATGCGTAAAAGATTTAATGGAGCGCGATAAA
                                                                                                                                                                                                     258 GTTTATCATTTAGCTAAAGAAAAAATGTGGGATATGCCAATTACAAATGCATTATATAGA 199
                                                                                                                                                                                                                                                                                                        318 ATGGATCAAGCATTATCTGAAATGAATATGGTTGTTGAAGGTATTTATACAACTAAATCA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 AAAGCTGCATTAATGACTCGTGGCTTAGCGGAAATTAGTAGA-----TTAGGTGAAAAG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 AAAAATATCATCGCAGTAGCAAGTGGTATCGTAGCTGGAATTGGCTACGGTGATAATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCACATCAACACATTCTCGGAATTTCACATTAGGATATAAACTTGGACAAGGTGAATCA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATTATTTGCGTGTACACGAATGATGACTTGATTGGTGTTGAACTTGGTGGTGCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAGGTGCCGATCCTATGACATTTCTAGGTTTAGGTGĞTATCGĞTGACTTAATCGTTACT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGT 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.2%;
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Pred. No. 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 918;
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RESULT 24 ABL34155/c ID ABL34:

ABL34155 standard;

DNA;

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ABL34155

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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibronatosis, rheumatoid arthritis, psoriasis and inflammaţory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15548 BP; 4209 A; 247 C; 2903 G; 8189 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000DE-01032529; 01-SEP-2000; 2000DE-01043826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune system disease; cytosine methylation; antiasthmatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                         13295 CTĀĀĀĀTĀTĀTĀTĀTĀĀĀĀĀTĀTĀTĀTĀTCTĀĀĀĀTĀTĀTĀTĀTĀĀĀĀTATATCTĀĀĀĀ
                                                                                                                                                                                                  477 TTAATATATTTCAAATTTATTATATACTACTCATCATATTTAGCATAATATCACATCTGACA 536
                                                                                                                                                                                                                                                                                                                                                                         237 ACTCTTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAACTGTATT 296
                                                                                                                                                                                                                                                                                                                                                                                                             981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                      TTCTTTATTCGACATACATATTAAAATCAATCAAAACAAAATAATAGTACTATCTAATTA 416
                                                                                                                                                               ATAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAGACACTTAACTTA 476
                                                                                                                                                                                                                                                                        CATATAAAACACATACGTATAAAATATACATATAAAAATATACATATATAA-AACACATAA 13416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 153; DB 6;
Pred. No. 3.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 1185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 15548;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                               27;
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12157 CTÁTAAAÁATAACATATATATATAACATATAAAAÁTÁÁCATATÁAAAATAACATÁTÁAÁA 12098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12397 CATAACATATATATATATAACATATATATATATATAACATATATATATATATATATATATATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12457 TATACATAAAATATATATATATAACATATATACATAAAATATATATATATATATATATATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12577 ATAAAATATATACATAAAATATATATATATAAAATATATACATAAAATATATATATATAA 12516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12757 TATATATATACGAĀATATATATATATATATATATATATATĀĀĀATĀTĀTĀTĀTĀTĀTĀTĀTATATA 12698
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                                                                                1488 GTACTGTAAAACCACTGATATCATTAGCAAAAAACTTAATGTAGAACTA-CCAATTTGC 1546
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11391 AATTCCTTATTTTATCTCATCATTTAAATTTTA 11359
                                                                      11505 AATAAAATATAAAATAAAATAAATATATATTCCATTACATTACTT-----CTTTACAAA 11452
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                                                                                                                                                                                                                                                                                                                                                                            11741 ААГАТАААААТААААТАТААААНТААААТАААТАТАААТАТАААТАТАААТАТАААТАТА 11682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11981 ACATATÁÀAAĀÁTAAAATÁTATATAÁCATATÁAAAATAACATATAĀAAÁTÁAAATÁTAAÁÁ 11922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12097 ATAACATATAAAAAATAACATATAAAAATAACA----TATAAAAATAAACATATAAAAATAA 12042
                                                                                                                                                                                                                                                                                                    2147 ТБААБААБАТАСААТАСАСБТСАААТАААТТАААСАААТТТСТААТАТАТААССАССТАСТС 2206
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                                2387 TATCAAATTCTATAATACATCATATCCTTTTTA 2419
                                                                                                                                                                                                                                                            2207 TAAACATAGGAACCAATAGTATATCATACCTAAGTAAGATATCCCTACAGCATGTATCAA 2266
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                                                                                                                                                                                  ATAATAAAGAAAAATCGTTATGTATATTTATACAATTACAAAATTTCCAACTTCAACAAC 2326
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                                                                                                                                                                                                                                                                            RESULT 25
                                                                                        Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                WO200277272-A2
                                                                                                                                                   Haematopoietic cell proliferation disorder related DNA sequence #240.
                                                          Homo sapiens.
                                                                                                                                                                                  16-JAN-2003
                                                                                                                                                                                                                                             ABZ10100 standard; DNA; 8056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 28; SEQ ID NO 240; 117pp; English.
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Piepenbrock C, Adorjan P, Grab,
A, Lipscher E, Maier S, Model F,
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                                                                                ACACCCTGTACTCTTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAAC
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                                                                                                                                       Conservative
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  1484 ACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATT 1543
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                                                         GTTATTÄTÄTTTAÄTTTÄATÄÄTÄÄÄÄÄÄÄÄÄÄÄTTTCGTTTTAAAAA-----AAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCATTG
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                                                                                                        ATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGAAGGA 1483
                                                                                                                                                                 GGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAA 1423
                                                                                                                                                                                                                                                                          CTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCATCATGTCTT 1363
                                                                                                                                                                                                                                                                                                                                                                            ---TAAAAATTATATTTÄÄATTTÄATÄTTTTÄÄTTTATATTTATÄATTTTAATATTTTÄ 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAATAGCAGAAGAAA 1004
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                                                                                                                                                          2437 TTCATACATAAATTATTATACATGCAATGTTTATTCAGAAACATTACACAATCCAAGAAT 2496
                                                                                                                                                                                                                 2746 TAAAAATAAAAAAATATTTAATCGTTTATTTTTAATAAATTTAAACGAATTTCGTTTAT 2805
                                                                                                                                                                                                                                                                    2377 AACACATAGTTATCAAATTCTATAATACATCATATCCTTTTTAAAAAGATGACTTCACAA 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                              2257 САТСТАТСАААТААТААГААБААААТССТТАТСТАТАТТТАТАСААТТАСААБТТТССАА 2316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1843 ATAAGTCAAATTAAACTTTTACTTATTTATAAAATAATATGTTTTGCACACTTTTTCACTA 1902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2023 AAATTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGT-----TTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1663 AAATATAGAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACA 1722
                                                   TTT 2499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGCCCATTAGTTCTTAATAAAATTGCTAATTACCCCAAAAAGGTTAAAAATACACATTCC 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATTAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 44.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to chemically pre-treated DNA of genes associated with apoptosis. The nucleic acids are used to allocate patients for specific therapy for HIV infection, Bloom syndrome, cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours and cancers. This nuclectide sequence represents a chemically treated apoptosis gene. Even SEQ ID numbers are the complementary DNA strands to the odd SEQ ID numbers. The sequence data for this patent is not represented in the printed specification but is based on information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6314 BP; 1514 A; 203 C; 1334 G; 3263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Seq ID #14; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis of associated diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-017444/02.
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus; renal ischaemia; amyotrophic lateral sclerosis;
5335 САААСАТТТААЛАТААААСТААТААТААСТААААСТААААТАТТСААТАТТТАСТАААА 5276
                                                                        290 CTGTATTCAAAGAATACCTCTTCTTCTTGTTCCATATCTTTTCCAATTATTTACAATAT 349
                                                                                                                                                                                                                                                                                                                                                     230 ACCCTGTACTCTTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAACCATTTTCTCAAATCTCCAATTTTAACATGCACAAGATTATTTAATGTAACAGAAC 229
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                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%; Score 148.8; DB 6; Length 6314; 44.9%; Pred. No. 1.5e-14;
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1487 AGTACTGTAAAACCACTGATATCATTAGCAAAAAACTTAATGTAGAACTACCAATT 1543 					1189 TGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAAAATTT 1248 4325 AATAAATCTACAAAAAAATAAAAAAAATTAAAAAAACTAAAAAA	1130 ACAATAAGTAATGAT-GTTCTAAAAATATATACCATCAAGATATTATAGGTGTACAGAT 1188 	1070 CTTCCTTGTAGTAGTAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCATTGATAGAA 1129	1010 CAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAGAACAT 1069		890 ATATGTACAACAAATACAACACAAACAGCATATGTGTAAAAATACTCCAATATTAATTTGT 949	830 GTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACAACAATTACGCACC 889		710 AACTTATGGGACGTGATCATAGAAAATATTACACATATAAACACTTACCGAAAAAATTTA 769	650 GGTGCAGGATCATTTGGCACGCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTT 709	590 ATATAATTITTGACTGGTTTCTTGATATAAATTAAGTTAAAAAAAATGAAAATCAGTATTTTA 649	530 TCTGACATGATTAACAATAGTAACACATTTCTTAACACTAGATAATATAAATAA	5099 TTACAAAAAAAAAAAAAAAAAAAAAAAACCTCTCTAAAAAA
RESULT 27 ACA18468 ID ACA18468 standard; DNA; 1020 BP.	QY 2502 ATTTACGGTGTAAT 2515 Db 3016 AACTAAAATACAAT 3003	QY 2442 ACATAAATAATTATACATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCA 2501	OY 2382 ATAGTTATCAAATTCTATAATACATCATATCCTTTTTAAAAAGATGACTTCACAATTCAT 2441	OY 2322 ACAACAAAACTCAAAGTTCTATTATAACAAATTCAAGAATTATATATA	QY 2262 ATCAAATAATAAAGAAAAATCGTTATGTATATTATACAAAATTTACCAAAATTTCCAACTTCA 2321	QY 2202 TACTCTAMACATAGGAACCAATAGTATATCATACCTAAGATAGTCCCTACAGCATGT 2261	QY 2142 CAATATGAAGAAGATACAATACACGTCAAATAAATTAAACAAATTTCTAATATATAACCACC 2201	QY 2082 CCATTAGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAA 2141 Db 3435 CAATAAATAATTATATTTAAAAAAAAATAATCTATCGACCGAAAAGGATAACTCACGCCTA 3376	QY 2024 AAITC-TATCATCCTTGACATAT-TTCAAACATAAAATATGATAAACTGTTTTTTTATGC 2081	QY 1964 TATTAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATA 2023	QY 1904 ATCATGTATATAATGAACATAATTTTACATAAAATAACTAATAAAAGAACGAATACATA 1963	QY 1844 TAAGTCAAATTAAACTTATTACTTATTATAAATAATATGTTTGCACACTTTTTCACTAC 1903	QY 1784 AATTATATAAACAAATTCCTATCTCCTATCTCAATTAACAATTGTTATCAGATTATAAA 1843	QY 1724 CCAACTAAGTATGTAACATATTACATAACATAACTAAGCTATAAGATTTCCTAGCT 1783	1664 3845	1604 3905	7 7 8 8 8 8 8 8

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the 6213 antisense squences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (6) inhibited by the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or equired for proliferation, or that inhibits cellular proliferation of the pathway in which a proliferation-required gene or its gene product lies or a gene on which hat test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required cor of a compound that inhibits the activity of the strains is present in a culture or acids are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang L,
Wall D,
                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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25-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; SEQ ID NO 6338; 1766pp; English.
                                     ftp.wipo.int/pub/published_pct_sequences
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Trawick JD,
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Forsyth RA,
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                                                     1587 ATAMAGCCATATCAMACATATTAT 1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1047 TTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAG 1106
956 AACAAGCAGCAAAAGAAATCATGT 979
                                                                                                                                                                                                                       836 GCATGATTGTGGAAGGTGTTTCAACAACTAAAGCAGCCTATGAATTGGCACAACAACTAG
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                                                                                                                                                                                                                                                                             TAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAACTTA 1526
                                                                                                           AAGTCGAAATGCCAATCACAGAAACAATCTACAATGTCTTGTACAATGACGAAGATGTAC 955
                                                                                                                                                              ATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAAATATATCACTAG 1586
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                                                                                                                                                                                                                                                                                                                                GGCGTGCGGGTAATTTATTAGGAAAAGGCCATAAGTTAGATGAAGTCTTAGAAAACATGG
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                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to CD prokaryotic cellular proliferation, their use in identifying the genes, and the discovery of novel antibiotics, the essential genes them use in the discovery of novel antibiotics, the essential genes coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent collectronic forms part of the printed specification, but was obtained in the form part of the printed specification, but was obtained in
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-020727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
                                                                                                                                                                                                                                                           Sequence 1023 BP; 344 A; 172 C; 237 G; 270 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-2000; 2000US-0257931F
16-FEB-2001; 2001US-0269308P
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                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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                                         689 TCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATA 748
                                                                                                                             629 AAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTG
                                                                                                                                                                          483;
    64 GCCGAAAATGGACACGAGGTCTGTATTTTGGGGAAATAAACCAGAGCAAATCGATGAAATA 123
                                                                                      4 AAACAAAAAGTÉGETGTTTTÁGGTECÁGGTTÉETGGGGGACÁGÉTTTÁGÉTEAAGTÁTTA 63
                                                                                                                                                                                            Similarity
                                                                                                                                                                          Conservative
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                                                                                                                                                                                            Score 148.4;
Pred. No. 1.
                                                                                                                                                                          Mismatches
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                                            Enterococcus faecalis DNA for cellular proliferation protein #64.
Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
                                                                                      13-FEB-2002 (first entry)
                                                                                                                                                                          AAS51287 standard; DNA; 1026 BP
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26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0245578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1026 BP; 346 A; 172 C; 239 G; 269 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           did not form part of the printed specification, but was obtained electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in prollieration, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct
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                                                                                                                              124 AAACACACCAACAACATTATTTACCAGAATTAATCTTACCTACTTCAATTCAGGCAACC
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                                                                                                                                                                       755 TACCGAAAAATTTAAAATATTTACCCACATATCTACCAGACAACATATATGCAACC 814
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                                                                                                                                                                                                                480;
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
CACAACAATTACGCACCATATGTACACAAATACAACACACAGCATATGTGTAAAAATA 932
                                           ACTGATTTAGCCACTGCTTTAGTAGATGTGGATGCGGTACTGTTTGTGGTACCAACTAAA 243
                                                                                    AGCAATATAGACGAAGTATTATCTGACAACAATAC - - ATGTATTATCTTAACTATTCCTA 872
                                                                                                                                                                                                                                                                                                   AAAGTCGCTGTTTTAGGTCCAGGTTCCTGGGGGACAGCTTTAGCTCAAGTATTAGCCGAA 63
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                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; noutropic; neuroprotective; anti-HIV; antionvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                      Homo sapiens
                                                                                neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 836.
                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                               ABL32863;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGCAGAAGAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTTGCTA 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATGCCAATCACAGAAACAATCTACAATGTCTTGTACAATGACGAAGATGTACAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6132 BP; 1642 A; 28 C; 1246 G; 3216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2001; 2001WO-EP007537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 836; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methylation.
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                                                                                                                                                                                                                 4683 AAAATATCCAATTATAAAAAAAAAAATAAAACTATTTCTATTTACAAATAACATAACTAT 4624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4623 ATACAAAAAAATCCCAAATÁATCCAACACAAAAACTAATAAAATTAATAAACAAATTCAA 4564
                                                                                                                                                                                                                                                                                                                                                                                       821 ATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACAACAA 880
                                                                                                                                                                                                                                                        641 AGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 ТАСТАСТАТСТААТТААТААДАДАТССТСАДТАСТТТАССАДСТАСДАДСТАСДАДТАТАД 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 ТТАСААТАТСАТАGAGTTCTTTATTCGACATACATATTAAAAATCAATCAAAACAAAATAA 400
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                                                                                    AAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACCAGCAAT 820
                                                                                                                                                                      ATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAAACACTTACCGA 760
                                                                                                                                                                                                                                                                                                   СТАТТСААТАТТАСАС--ТААААТТССТАААСААЛАСААТТАААТААААЛАТААААААА
                                                                                                                                                                                                                                                                                                                                            АТАААТААТАТАТТАТТТТТБАСТБGTTTCTTGATATAAATTAGGTAAAAATGAAAATGAAAATC 640
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1898 CACTACATCATGTATATAATGAACATAAATTTTACATAAAATAACTAATAAAAAGAACCAA 1957
                                                               3497 AATAATACTCAACATCATTACTCATAAAAAAAATATAAATCAAAACCATATAACATACTA 3438
                                                                                                        1838 TATAAATAAGTCAAATTAAACTTTTACTTATTTATAAAATAATATGTTTGCACACTTTTT 1897
                                                                                                                                                                                          1778 CTAGCTAATTATATAAACAAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGAT 1837
                                                                                                                                                                                                                                      1718 TAACATCCAACTAAGTATGTAACATATTACATAACAAACTTAAGTATAACTTAAAATTTC 1777
                                                                                                                                                                                                                                                                                                                        3797 ААТТСТТАРАТТТРАСАССРАРАЛАСАСАРАРСАРАНСРАДИВАРТРАРАТТАРТ 3738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1538 ССААТТІВСАТАЎСТАТТІАСААТТІАТЛАСАТВАВАЛАТАЎАТСАСТАВАТАААВССАТА 1597
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                                                                                                                                                                                                                                                                                                                                                                 1658 GTCAAAAATATAGAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGT 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4037 ТТТААТТТТТААТАЛААААТТАТСААЛЛАААТСТТАЛАСАТТСААТАЛАЛАЛААЛАТТАТА 3978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941 TTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAATAGCAGAA 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACCTTATATCACATACAATAATTAATTTAAAATTAAATCAATCCTAAATATAAAAACCA 3858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACT 1419
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                                                                                                                                                      CAAAAAACTTAAATCAACATTTCTCCAAAAAAATATATACGAATAACCAACAACACATAA 3498
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RESULT 31

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Tragment Name
WP Sequence split into 31
WP ABC69245_00
WP ABC69245_02
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1329 TAGATCTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAA 1388
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                                             CACTAATGACACGCGGAATGGCTGAAATTACTCGTCTCGGAGTTGCTGTGGGCTCTA---
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                                                                                                     TTATCGCACTTGGCGCAGGAATCTCTGATGGCCTTGGATACGGCGATAATGCTAAAGCGG
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                                                                                                                                                              TACGTATTTATACGAATGATGATGTCATCGGTGCTGAAATTGGTGGAGCGCTTAAAAATA
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                 Query Match 3.:
Best Local Similarity 49.0
Matches 484; Conservative
                                                                                               The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                       Sequence 319630 BP; 105207 A; 55428 C; 66726 G; 92263 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                      New genomic sequences from Listeria species, useful treatment and prevention of infection, also related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000; 2000FR-00012697.
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                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 7; 180pp; French.
                                                                                                                                                                                                                                                                                                           antibodies and modulators.
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CNRS CENT NAT
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               3.1%; Score 146.2; DB 6; Length 49.8%; Pred. No. 4.5e-14; ative 0; Mismatches 473; Indels
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52711 GTGTGCATTCACGTAATTGGCGTGCTGGAAACATGCTCGGTAAAGGCGAGAATTTAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1389 CAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATA 1448
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GTTGGGCGAAAAAACTAGATATTGATATGCCAATTACCGAATCGATTTACGCGATTTTAT 52890
                                                                                                 CATTAGCAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTAC 1568
                                                                                                                                                                                                             AAGTTTTAGAAAAATGGGTATGGTCGTTGAAGGTGTGCGTACAGCCAAAGCAGTTCATG
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cc cytosine methylation state and/or single nucleotide polymorphisms (SNPs)

Cl in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription cc (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, cc haematological disorders, immunological disorders, Werner syndrome, cc haematological disorders, neurodegenerative disorders, Warner syndrome, cc neurological disorders, neurodegenerative disorders, Warner syndrome, syndrome, neurodegenerative disorders, Warner syndrome, cc neurological disorders, neurodegenerative disorders, warner syndrome, cc infarction, hypertension, angiogenesis, erythropoiesis, congenital heart cd disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours cor cancer. Sequences ABK28127-ABK28472 represent DNA transcription cassociated genomic DNA molecules of the invention. Note: The sequence data for this patent did not form part of the printed specification but of first of the printed specification but confidence of the confidence of the syndrome of the sequence confidence of the syndrome of the confidence of the syndrome of the printed specification but confidence of the syndrome 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the
                                                                                                                            Sequence 11745 BP; 3183 A; 270 C; 2383 G; 5908 T; 0 U; 1 Other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 206; 32pp; English.
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07-APR-2000; 2000DE-01019173
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01-SEP-2000; 2000DE-01043826
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                                                3.1%; Score 145.4; DB 6; 43.5%; Pred. No. 5.2e-14;
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  1406 ATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAAC 1465
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                                                                                                                                                                                                     ATGAATGAAATTAAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTA 1345
                                                      ATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAAT
                                                                                                                                                       GGAATAATCGCTGGAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAACTAAAGGC
                                                                                                                                                                                                                                                                                                                                                          ACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAAATAATATACCATCA 1167
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                                                                                                                                                                                                                                                                                                                                                                                                        AGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACAT--AATTGCAATTGCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATA 807
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2485 CAATCCAAGAATTTTCAATTTACGGTGTAATGCTGAACGTTCCATTCCAACAAATTCAGC 2544
                                                                                                                                                               2425 ATGACTTCACAATTCATACATAAATAATTATACATGCAATGTTTATTCAGAAACATTACA 2484
                                                                                                                                                                                                                                                        4004 АЛАЛАЛАТАСТТАСАЛАЛАТАЛСТТТАЛАЛАЛАСЛАТТАЛАЛАЛТЛАЛАЛТТАЛАЛАС 3945
                                                                                                                                                                                                                                                                                                                                    2365 ATATACTTCACCAACACATAGTTATCAAATTCTATAATACATCATATCCTTTTTAAAAAA 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2305 CAAAATTTCCAACTTCAACAACAAAACTCAAAGTTCTATTATAACAAATTCAAGAATTAT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2186 TTCTAATATAACCACCTACTCTAAACATAGGAACCAATAGT-ATATCATACCTAAGTAAG 2244
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1414 TGGACTAGAAATAGGAAAATATAAATACATTAATAGATCACAAACCTAAAGCT 1473

1354 ATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTT 1413

1294 PATTEAPARACKITYTATATRAGCAPARARTICATTCARTKATTCTTCATTCATTCATTCATTGGTCC 1353

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Matches 556;
                             Query Match
                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatorid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                Sequence 7597 BP; 1965 A; 109 C; 1790 G; 3733 T; 0 U;
                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; anti-HIV; anticonvulsant; ophthalmológical; antifheumatic; antiattic; antidabetic; antipporiatic; antimentator; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 986; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17.
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO:
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                  Similarity
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                Score 144.2; DB 6;
Pred. No. 7.9e-14;
Mismatches 613;
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                                          2431 TCACAATTCATACATAAATAATTATACATGCAA 2463
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                                                                                                                                                                                                 2072 TTTTTTATGCCCATTAGTTCTTAATAAAATTGCTAATTACCCAAAAAAGGTTAAAATACAC 2131
                                                                                                                                                                                                                                                                                                                  2013 СТGAСАТААТААТТСТАТСАТССТТGAСАТАТТТСАААСАТА-АААТАТGAТAAACTGT 2071
                                                                                                                                                                                                                                                                                                                                                         1953 ACCAATACATATTAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTC
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                                                                                                                                                                             1654 AACGGTCAAAAATATAGAATACAACGTTCACCACATATATAAAAAAGCAGTCAAATACCCA 1713
                       133 AAAAAATACATAAATAAAAAAATAAATAAATAA 101
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Best Local 9
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01-SEP-2000; 2000DE-01043826
                                                                                                                                                            European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                Match 3.0%; Score 143; DB 6; Length 47108; Local Similarity 43.6%; Pred. No. 1.3e-13; s 1181; Conservative 0; Mismatches 1495; Indels 31
                       482 ATATTTCAAATTTATTATACTACTCATCATATTTAGCATAATATCACATCTGACATGATT 541
                                          422 AAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAGACACTTAACTTATTAAT 481
                                                                               362 ТАТТССБАСАТАСАТАТТАРАРАТСАРАТСАРАРАСТАРТАРТАСТАТСТРАТТАРТАРА 421
                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
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RESULT 35 ABK31511/c

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the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABX31158-ABX31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or this patent did not form part of the printed sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
Sequence 47108 BP; 15349 Å; 429 C; 8736 G; 22594 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 354; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to chemically modified DNA sequences of
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	1550 TCTATTTACAATTTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTA 1609	1490 ACTGTAPAACCACTGATATCATTAGCAAAAAACTTAATGTAGAACTACCAATTTGCATA 1549		CTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGA	1317 AAAATCATTCAATAGATCTTCATACATTAATTGGTCCATCATGTCTTGGAGAT 1369	1261 TGTTGCTACTGTTATAACTAAAGGCATGAATGAAATTAAAACACTATATATA	1201 AAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAAATTTAAGGTAATAATGC 1260 	1141 TGATGTTCTAAAAATAATATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATT 1200	1081 TATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAA 1140	1021 AATTITTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAG 1080	962 GAAATTACATCACTCAAATTTCCCAGTGAAATAGCAGAAGAAATTTTACAA-TATAATCC 1020	902 ATACAACAACAAGGATATGTGTAAAAAATACTCCAATATTAATTTGTAGTAAAGGTAATC 961	842 AACAATACARTGTATTATCTTAACTATTCCTACACAAATTACGCACCATATGTACACAA 901	782 ACATATCATCTACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGAC 841		662 TITGGCACAGCAATAGCAATIGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGA 721	602 ACTGGTTTCTTGATATAAATTAAATTAAAATGAAAATCAGTATTTTAGGTGCAGGATCA 661	542 AACAATAGTAACACATTTCTTAACACTAGATAAATAAATA
QY 2687 ACTGGTAAATCTTTTGCTGTAATCATCTCCTTAGGAGATTTCATAATTAAAATCCATTCT 2746	Db 7328 AATACTACAAATCAAATAAATTAAAAACGTAACGAATACAATAATTAAT	7388 AAACGAAAAATTCTAATACCCTAAAATTCAAATAAATAAA	Db 7448 AAAAATAAAACGAAACTAATAAAAATCTAAAAAAAATATACTAATAAAAAAA	7508 CATAAAAAAAATAAATTCCCAAAAACTAAACCTTCAAATACCCCAAAATTTAAACGTTAA 2507 CGGTGTAATGCTGAACGTTCCATTCCAACAAATTCAGCAGTTCGTGATACATTTAACCTCCA	OY 2387 TATCAAATTCTATAAATACATCATATTTAAAAAAAAAA	2327 7627	OY 2267 ATAATAAAGAAAATCGTTATGTATATTTATACAATTACAAATTTCCAACTTCAACAAC 2326 DD 7687 TCAATTTAAAATACCTTAATAACATTCAAAAAAAAAATACTAAACAATTAAATTCAC 7628		2147 TGAAGAAGATACACGTCAATAATTAAACCAATTTCTAATATAACCACCTACTC	QY 2087 AGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAACAATA 2146 1 <t< td=""><td>OY 2027 TOTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTATGCCCATT 2086</td><td>1967 TAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATAAAT </td><td>1907 ATGTATATGAACATAATTTTACATAAAATAACTAATAAAAAAAA</td><td>QY 1849 CARATTRARCTTTTACTTATTATAARATAATATGTTTGCACACTTTTTCACTACATC 1906</td><td>CY 1789 TATAAACAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATTATAAATAA</td><td>QY 1730 AAGTATGTAACATAATTACATAACCAAACTTAAGTATAACTTAAAATTTTCCT-AGCTAATTA 1788 </td><td>OY 1670 GAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACT 1729</td><td>Db 8346 CTAAAAACTACCCCTTATAAAACCATTATAAAAAATAAAAAA</td></t<>	OY 2027 TOTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTATGCCCATT 2086	1967 TAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATAAAT 	1907 ATGTATATGAACATAATTTTACATAAAATAACTAATAAAAAAAA	QY 1849 CARATTRARCTTTTACTTATTATAARATAATATGTTTGCACACTTTTTCACTACATC 1906	CY 1789 TATAAACAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATTATAAATAA	QY 1730 AAGTATGTAACATAATTACATAACCAAACTTAAGTATAACTTAAAATTTTCCT-AGCTAATTA 1788	OY 1670 GAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACT 1729	Db 8346 CTAAAAACTACCCCTTATAAAACCATTATAAAAAATAAAAAA

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The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis associated genes (II) having sequences (AB066971-AB0679178) or their complements (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis,
                                                                                                                                                                                                                                                                    New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g
diagnosis or treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                              Claim 1; SEQ ID NO 100; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-500450/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenesis associated polynucleotide SEQ ID NO 100.
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diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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E. faecium DNA sequence SEQ ID 1399
                                01-JAN-2004
                                                                                                  ADC91772 standard; DNA; 1062
                                                                                                                                                                                      1071 ATAATAACACATACATTTAAAAAATTTATTT 1041
                                                                                                                                                                                                                     2474 GAAACATTACACAATCCAAGAATTTTCAATT 2504
                                                                                                                                                                                                                                                                                     2234 ACCTAAGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTATAT 2293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1491 AATAAAAATACCGTTAAAAATATCTTTTAATTÄÄTCAAÄTACATÄTTTÄTAATAÄÄÄAT
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                                                                                                                                                                                                                                                                                                                                                      1251 AATTAAAATTTACCTATTATAAAACTATACATTTÄATATTÄAATTACTCTTATCAATAAA 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1761 СТАТААСТТАЛАЛІТТССТАССТАЛІТАТАТАЛАСЛАЛІТССТАТСССТАТСТСЛАТТА 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1850 TAAAAATAAAACAATTTCTACAATCCTCCAAAATTCTAAATATTACATTTACCTAAATAA 1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001 TACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATAAAATA 2060
                                                                                                                                                                                                                                                                                                                       AAAATCATTCAACCTCTTATÄČČTTTÄTCTTTCTÄTAÄÄÄÄACAAÄACTAÄTÄTČÄCCTAČ 1132
                                                                                                                                                                                                                                                                                                                                                                                                                          ТТАТАСААТТАСААААТТТССААСТТСААСААСААААСТСАААGTTСТАТТАТААСАААТ 2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAATTTCTAATATAACCACCTACTCTAAACATAGGAACCAATAGTATATCAT----- 2233
                                                                                                                                                                                                                                                      САЛТАТСТТАРАТАРСАТТАРАЛАЛТСТТАТТРАТТРАТТТЕСТАРСАНСЕТТАТТАРАЛАРАЛ 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACATAATTTTACATAAAATAA 1940
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New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                ds; gene; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                                                                                                                                                                           02-JUL-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                   30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                Enterococcus faecium.
                                                                                                                                                                                                                      P-PSDB; ADC95426.
                                                                                                                                                                                                                              WPI; 2003-799836/75.
                                                                                                                                                                                                                                            Doucette-Stamm LA,
                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                  24-JUN-2003
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98US-0085598P.
                                                                                                                                                                                                                                                                                                   98US-00107532
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CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having CC one of 10 fully defined sequences given in the (or comprising 40 CC sequential nucleotides chosen from any of the nucleic acids, its CC complement or sequences hybridising to it). Also included are a CC recombinant vector comprising the nucleic acid operably linked to CC transcription regulatory element, a cell comprising the vector and a CC single-stranded probe comprising the nucleic acid. The nucleic acids are CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions CC resulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans condexived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents cone if the disclosed E. faecium nucleic acids. The invention relates to an isolated nucleic acid derived from

Example 1; SEQ ID NO 1399; 243pp; English.

Sequence 1062 BP; 362 A; 204 C; 246 G; 250 T; 0 U; 0 Other;

Query Match

Local

Similarity

49.6%;

Score 139.8; DB 9; Length 1062; Pred. No. 3.6e-13;

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  293
                                        885 GCACCATATGTACACAAATACAACACAAACAGCATATGTGTAAAAATACTCCAATATTAA 944
                                                                                                                                                                            116 ACGTTCGGATTTGGGGGACATCGTGCTTCACAAGTAGAAGAAATCAACACCCAACACACGA 175
                                                                                                                                                                                                                                                                                                           705 CAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAAA 764
                                                                                                                                                                                                                                                                                                                                                                                                       645 TTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATAT 704
                                                                                                                                                                                                                                                                                                                                                           56 TTTTÁGGACCÁGGCTCTTGGGGTACTGCTTTGGCACAAGTCCTCGCCGAAAACGGACATG 115
                                                                                                                               АССАЛСТАТТАТСТСАСЛАСААТАСАТСТАТТАТСТТААСТАТТССТАСАСААСААТТАС 884
GTTCTGTTGCAAAAGAACTAGTGCCTAAA-----TTGAATACAAAGCCAGTGATCATCC 346
                                                                                   AAGATGCAGTAAAAGÁCGCAGATGC---GGTGCTATTCGTCÁTTCCAÁCGAAAGCAATÁC
                                                                                                                                                                                                                     ATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAG
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04-OCT-2000; 2000FR-00012697
                                             04-OCT-2001; 2001WO-FR003061.
                                                                                                                                                                                                                        Antibacterial; Listeria; food contamination; mutational analysis; infection; ds.
                                                                                                                                                                                                                                                                                                                                    29-AUG-2003
29-AUG-2002
                                                                                          11-APR-2002
                                                                                                                                                                                                                                                                                      Listeria monocytogenes 4b contig DNA sequence #747.
                                                                                                                                                                                                                                                                                                                                                                                                      ABQ70805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABQ70805 standard; DNA; 2791 BP
                                                                                                                                   WO200228891-A2
                                                                                                                                                                              Listeria monocytogenes ATCC 19115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1001 CÁAAÁGÁAÁTCATGT 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1536 TACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAGCCA 1595
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2791 BP; 942 A; 450 C; 622 G; 777 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 3618; 180pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 2.9%;
Local Similarity 49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          844
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                     TGCGTATTTATACGAATGATGATGTGATTGGTGCAGAAATTGGTGGCGCGCTGAAAAATA 1259
                                                                TAAAAATAATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGCATATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATATTACACATATAAACACTTACCGAAAAATTTAAAAATATTTACCCACATATCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGGACGTGATCATAG
                                                                                                           CGAGCTGTAAAGATTTATCAGCTGCTGAAATTGTTCAAGATCGTTTCATCAATAATAATA
                                                                                                                                                      TTGCTGGTGATAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTC 1148
                                                                                                                                                                                                 TTCTTTCTGGACCAAGTCATGCGGAAGAAGTTGCGCTTCGTCATCCGACAACACTTTGTG 1139
                                                                                                                                                                                                                                                                                      TTCGAATGTCCGAAGTGATTGAAGACGAAATAGATGCGTCCAAACGTAAAGCGCTTGTTG
                                                                                                                                                                                                                                                                                                                                    ACTCAAATTTCCCAG----TGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTA 1028
                                                                                                                                                                                                                                                                                                                                                                               GCTAAA-AGAACCAACCATTTTAGTGCATGTGAGTAAAGGTATTGAACCAGAAACAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCAACTGAGGTAAAAGCGACATTGTCACTTGATGAAGCTATTGATGGTGCAGAAAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTGTGAATGAAATTAACGAATCGCACACGAATAGTCACTATTTGCCAGATATTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTGCACTTGTCCTAGCTGATAATAATCATCAACCAGTTATTTGGGGGAAACTTAGATAA
                                                                                                                                                                                                                                            TACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTCGTAATTGCTATTCCAACAAATGCGATGCGAATCGTTTGTAAGCAGTTAAATGAAGC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECH SCI.
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Pred. No. 3.8
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL33307 standard; DNA; 6175 BP.
                                                                          Claim 1; SEQ ID NO 1280; 32pp + Sequence Listing; German
                                                                                                                                                                                                                        WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAAAATAAA 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTATTAGAAAAATGGGCATGGTCGTTGAAGGTGTTCGAACAGCTAAAGCAGTACATG 1553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTGCATTCACGTAATTGGCGTGCTGGTAATATGCTAGGTAAAGGCGAGAATTTAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAATCCGCAAACATTTTACGGATTGACAGGTATTGGTGACTTAATCGTTACTTGTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGATCTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAA 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTAATGACTCGCGGGATGGCAGAAATCACTCGTCTCGGTGTTGC-----TGTTGGCT 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTATCGCACTAGGTGCAGGAATTTCTGACGGCCTTGGTTATGGCGATAATGCTAAAGCGG 1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6175 BP; 1506 A; 154 C; 1357 G; 3158 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5706 TACAAATATATATAAACAAATATATATAATAAATATAAAATATAAAACATATATATATAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5882 АССТРААССАААТАТАРААТАСАААТАТАРААТААТААТААЛАТАТАЛАТАРААСАРАТАТСРА 5823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 ACACATATAAACACTTACCGAAAAAATTTAAAAATATTTACCCACATATCATCTACCAGAC 799
                                                                                                                                                                                                                                                                        CACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAA 1519
                          TATAAAAATAAA-CAATATAAAATATATAAAACAAATATTTTATACAAACATATATAAAC 5112
                                                                       TCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTCAA 1639
                                                                                                                                                                                                                           AAATATATACGTATAAAAČCTAAATAACGTAAAATATATATAAACAAATATATACGTACAA 5291
                                                                                                                                                                                                                                                                                                                                                                                                                       ACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TÄTÄÄÄÄTÄTÄÄÄACATÄTÄTÄÄÄÄÄTÄTÄÄÄCATÄTÄÄÄÄTÄÄÄÄTÄTÄÄÄTÄTÄÄÄÄÄTÄT
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Pred. No. 5.2e-13;
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Human; angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds;
                                                     Human angiogenesis associated polynucleotide SEQ ID NO
                                                                                                                                                             ABQ66998 standard; DNA; 37515
                                                                                                                                                                                                                                                  4296 AATAC 4292
                                                                                                                                                                                                                                                                                      2479 ATTAC 2483
                                                                                                                                                                                                                                                                                                                                                                                                                             2359 AATTATATATACTTCACCAACACATAGTTATCAAATTCTATAATACATCATATCCTTTTT 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2299 CAATTACAAAATTTCCAACTTCAACAACAAAACTCAAAGTTCTATTATAACAAATTCAAG
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                                                                                                                                                                                                                                                                                                                           AAAAAGATGACTTCACAATTCATACATAAATAATTATACATGCAATGTTTATTCAGAAAC 2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAATATAAACATAAATAAATAATTACATTATATTTAAACATAAATAAATAAATATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACATAATTTTACATAAAAT 1938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAATATATAAACCTAATATAAAATATATATAAACAAATATAAATAAACATATAAATATATA 4992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATTACATAACAAACTT 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AĀATĀTAĀACĀĀATĀTAATTATĀĀĀĀĀCCTĀATĀTĀĀĀĀTATĀĀĀCĀĀĀTĀTĀTĀĀĀĀCĀ 5052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATAAAA 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATACAATATAAATTTAAACATATAAATAAATACAAACATATAAATAAATATATCGTATA 4755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nuclectide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarteriosclerotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37515 BP; 11428 A; 425 C; 7165 G; 18497 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 28; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis or treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-500450/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2000; 2000DE-01061338.
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525 TCACATCTGACATGAT-TAACAATAGTAACACATTTCTTAACACTAGATAATACAATA 583
                                                                                                                                                                                                                                                          165 AGAAGCAAACCATTTTCTCAAATCTCCAATTTTAACATGCACAAGATTATTTAATGTAAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                        AATCTTAAATAAATAATTAAAAAAATCTCACTAAAAAATACTAAACCAATTCCCAAAA
                                                                                                            ACTATCTAATTAAAAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAG 464
                                                                                                                                                                                                                        AATACATACTAAACTCTTACACTATACCT-AATATTACTATAAACCTCGAAAATATAACA 18730
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1660 CAAAAATATAGAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCCATCGTTA 1719	1600 AAACATATTATCTTAGTCTATCATCCTTTGATAATTTCAACACAATGATAAATAA	ACATCTCCAAACTCAAAACTATTAAAATTCTAAAAAAAA	17539 AAAAATAAAAAAAAAAAAAATACCTATA-AATAACAATAAAAACTCAAAAAAAA	AGGAACCAGTACTGAAAACCACTGATATCATTAGCAAAAAAAA	1420 AGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGA 1479 	1360 TCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACT 1419	1300 AACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCATCATG 1359	1240 AAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAACTAAAGGCATGAATGA	1180 TGTACAGATTGGACCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGG 1239	1120 ATTGATAGAACAATAAGTAATGATGTTCTAAAAATAATAATATCCATCAAGATATTATAGG 1179	1060 TGCAGAACATCTTCCTTGTAGTATAAGAACTTGCTGGTGATAATAAGAACTTGGTGAATC 1119	1000 AGAAATTTTACAATATAATCCAATTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAAT 1059 .	940 ATTAATTTGTAGTAAAGGTATCGAAATTACATCAACTCAAATTTCCCCAGTGAAATAGCAGA 999	880 ATTACGCACCATATGTACACAAATACAACAGAAACAGGATATGTGTAAAAATACTCCAAT 939	820 TATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACAACA 879	760 AAAAATTTAAAATATTTACCCACATATCATCTACCAGACACATATATGCAACCAGCAA 819	700 TATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCG 759	644 ATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGG 699	584 AFFAATAFATATTTTGACTGGTTTCTTGATATAAATTAGGTAAAAAATGAAAATCAGT 643
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2/40 CATTCTATACAT-TRUGTAATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATTG 2/38	TTTTATTTTAACTTAATTAATAAATAATAATAATCACTATATCAACAA	16412 AACCTAAATAAACTAAATACTTTACTAATAATAATAAATAAT	2620 ACGTAATGGTACAGAAATAACTTTAGCACTTAAAACATCATTAATAGGCGAATTAGATAC 2679	2560 ACCTCCAAAACGAGATAACTGAGTTTTTAAATACTGTCTTTCAAATTCTTCACGAGCTTT 2619	2500 CAATTTACGGTGTAATGCTGAACGTTCCAACAACTTCAGCAGTTCGTGATACATT 2559	ATACATAAATAATTATACATGCAATGTTTATTCAGAAACATTACACAATCTAAGAATTTT	ACATAGTTATCAAATTCTATAATACATCATATCCTTTTTAAAAAGATGACTTCACAATTC	2320 CAACAACACACAAGTTCTATTATAACAAATTCAAGAATTATATATA	GTATCAAATAATAAAAAATCGTTATGTATATTATTACTACAAAATTCCAACTTTATTAAAAACTTTATACTAC	CTACTCTAACATAGGAACCAATAGTATATCATACCTAAGTAGTATCCTCCTACATAGATATCCTACACATAGTATATCATACATA	ACCATATGAGAGATACATTACACGTCAATTAACTAATTTCTATATTACACTATATACACTTAACCACTAACGATTATACCTAAAAAAAA	ATCTTAAAACACTCTTAACTCCAAATAATTAAAATAATTACCTAAAAAA	AATAAATTCTAFCATCCTTGACATATTCAAACAATATGATAAAATTATAATAATAATAATAATAAATA	CATATATTACATACACACCTATTTACTACGTAGATATTACATAGATGTCCTGACAT ACTTACTCTTAATTCTTAAAAAAAAAA	CTCAAAATAATAATAATAATAATACTATCAATAACTAAAAAA	1840 TAAATTAAACTTTTTTTTTTATTTATTAAAATTTTCA 1899 1840 TAAATTAAGTTAAACTTTTTCA 1899 1870 TTAAACTTCTTATAAAACTAATAAAAAAAAAAAAAAATAAAATTAAATCTTTAAAAT 17123	ATACABAACCTTCTAABAATTABAAATATTABAABAAATBAAAATACATCTABABAATC	ACCACAAAAATTAAATTTTCTAAAATTATAAAAAAAATAAAAAA	

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3679 TAACCATATATCCAATAATACAACATCAGGCTCTTTTTCATAAGCCATCTTGATCGCGGA
3619 ATAAGGATACCTTTCTTAAGCTTTTCCAGTACACTTAATCCAGTATATCAGATCCAGTCTCT
3559 ATGCAGAGACTTTACAGCAGTGGCAATATTACCATGCCCACTAATCATAACAGGCAA
3499 TACAACTAACTTTAATCTTCCTTCTGTAAAAGGCTTTTCTATATATCATAAGCACCCAT
3439 AAATGCTGATTTCAACTCATCATTTTCTCTACGTAATCTACGAGACTCTATAGCTCTCTT
3379 ATTAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTATTTCATAATCCTC
3319 TICCTTICCAACACCTGGCGAACCAGTAATGAGTATACGACTCGATGTAGTAGCTGCTTT
3259 CATAGATATAAATGGAGTATCATACCCCTTGGATTTTTTATGTATTAGCCTAGCAACTAC
3199 ACTITICCICACTACCAAATATATTAACCAAGTAATTATTAGCTGGTAGCATAGATGAGTA
3139 AIGATTIGCTIGCTCTATAATTCCAATAIGAGGAGGTACICTATGAGACAATATATTATT
3098TOGTATCGTAAATCTTTCATCTATAAATAACGTACCT
3039 TACTATITICCCTATATATITTTCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTA-
2979 CACTITCAATATCTITGGAAGAAGACACAATAATTCTCACATCTATACTAACAGGAATCT
2919 TAATTGGAAGGACATTTAATCTATAATATAAATCCTCACAAAACCTACCAGCTTTTACTT
2859 TCATAAAATACCTACACAATTCCGGTATATCTGTACAATATTCTACTAAAGACGGTACTC
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14572 CTARACGARTATTARTTARAAATTATARAATATTARAAATATT 14531
                                                                                         14632 TTCTAAATTTACCACTTCTACTATAATATATTTTTTCAAATTTCTACCGATAATATTAAA 14573
                                                                                                                                                                                   14692 AATAAAAATTTTATAAAACAATATAAACTATAAATTCATAACACAATACCAATATAAAAATT 14633
                                                                                                                                                                                                                                                                                                                                                                        14925 AAAATAĀĀĀĀĀĀĀĀTĀTĀĀAAAACTATĀĀCCTTTĀAAAAATĀAAĀATTĀATĀĀTĀ 14866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15155 TACTTCTCTTTÄÄTTTTTCATATĆ-----TAAAAAĆTÄTTTTÄTTÄTTCCGTTAT 15106
                                  4457 ATCAACAATAATATGTCCAAAACTATCAATGATAGAATTTTT 4498
                                                                                                                                      4397 TAGATGAGTTAACGCACCATCTCCATGTATTGAAGTCAAATCATCCCCGTATATTACAATT 4456
                                                                                                                                                                                                                                  4337 GATAGATGAAACCATACCACCAACAAGAGTATTATCATTGACTACTTCACGTATAAAATC 4396
                                                                                                                                                                                                                                                                                                                    4277 TAATTTTATATTTAAACCACTAGACAAATAATATCCCCACCAATGACTATCAACATATGT 4336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4097 CTTAATAAAAACTTATCAACTTTGTAAACCTATAGTAACTAATTATTAATAAATTA 4156
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 0000 172.8 172.8 172.8 1770.8 1770.6 1770.6 1769.2 1768.8 1768.8 1768.8 182.2 182.2 181.4 180.2 175.8 174.4 173.8 173.8 173.8 173.8 173.8 173.8 173.8 173.8 371 357.6 338.6 231 219.6 219.6 207.8 188.6 186.4 168.4 167 166.8 166.4 166.4 166.8 Score Query 100.0 100.0 29.8 20.7 12.6 7.8 19517 19517 175559 13124 13147 254050 3900 5 133877 5 349751 9 19517 9 172816 8 14867 8 300205 8 12229 8 12227 7 33275 7 104992 7 104992 7 104992 7 104992 8 30155 8 3015 11400 4 349980 3 349174 279110 1 12477 9 23906 Length DB DMU11584 DMU37541 AC093899 PVGLNABC AX599046 AE011408 AB080665 AX344555 AB063522 AF308670 AC120883 Homo sapi AL035476 Plasmodiu AX625666 Sequence AL031746 Plasmodiu U37541 Drosophila AC145101 Homo sapi AE009105 Agrobacte AE008070 Agrobacte AL029358 Plasmodiu AX599046 Sequence U11584 Drosophila U37541 Drosophila U37541 Drosophila AC093899 Homo sapi AE001594 Clostridi AC127383 Homo sapi AC127383 Homo sapi AC127383 Homo sapi AE010598 Fusobacte AP004827 Staphylou AC004157 Plasmodiu AC004157 Plasmodiu AE015939 Clostridi AP003134 Staphylou AE015939 Clostridi AP003134 Staphylou AE015938 Clostridi AP003136 Staphylou AE015938 Clostridi AP00377 Campyloba AR377574 Sequence AE007680 Clostridi AP3007680 Clostridi AF308670 Cowdria r AX685245 Sequence AX685247 Sequence AX685247 Sequence AX685250 Sequence AX68526 Sequence AJ235272 Rickettsi AE018640 Rickettsi AE011408 Leptospir AB011408 Leptospir AB011408 Leptospir AX344555 Sequence AB063522 Wiggleswo X68129 P.vulgaris Description

	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION					DEFINITION	Locus	AF308670	RESULT 1
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.	Ehrlichia ruminantium	Ehrlichia ruminantium (heartwater rickettsia)		AF308670.1 GI:15811157	AF308670	partial cds.	complete cds; and hypothetical cell division protein ftsQ gene,	and hypothetical nitrogen assimilation regulatory protein genes,	gene, partial cds; hypothetical glycerol 3-phosphate dehydrogenase	Cowdria ruminantium clone 19hw hypothetical integrase/recombinase	AF308670 4750 bp DNA linear BCT 03-OCT-2001		

AL IGNMENTS

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REFERENCE
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Barbet, A.F., Whitmire, W.M., Kamper, S.M., Simbi, B.H., Ganta, R.R., Moreland, A.F., Waangi, D.M., McGuire, T.C. and Mahan, S.M.
A subset of Cowdria ruminantium genes important for immune recognition and protection
Gene_275 (2), 287-298 (2001)
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RNLRSMINKAATTSSRILITGSPGVGKEVVARLIHKKSKGYDTPFISMYSSMLPANNY
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3121 ATCTATAAATAACGTACCATGATTTGCTTGCTCTATAATTCCAATATGAGGAGGTACTCT 3180	<u>-</u>	2041 CATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCCATTAGTTCTTAATAAAA 210	Ş
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TRCATGAGTACACACCTATTTTTTTACAGATGCTATTCATAAATACCTACACAATTC) B &	1741 ATATTACATAACAAACTTAAGTATAAACTTAAAATTTCCTAGCTAATTATAAACAAATT 1800	유 성
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2281 TOSTTATOTATATACAMATTACAMATTTCCAMCCACAMACTCA
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3421 GOCAMITADARCOCCANTACTARACTARACTARACACACACACACACACACACACAC

2707 AATCATCTCCTTAGGAGATTTCATAAATTAAAATCCATTCTATAACATTACGTAATTGTCT 2	Qy 2647 ACTTAAAACATCATTAATAGGCGAATTAGATACTATATCTACTGGTAAATCTTTTGCTGT 2706	QY 2587 TAAATACTGTCTTTCAAATTCTTCACGAGCTTTACGTAATGGTACAGAAATAACTTTAGC 2646	OY 2527 CATTCCAACAATTCAGCAGITCGTGATACATTACCTCCAAAACGAGATAACTGAGTTTT 2586	2467 TTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTACGGTGTAATGCTGAA	Query Match 29.8%; Score 1416; DB 6; Length 1416; Best Local Similarity 100.0%; Pred. No. 1.3e-169; Matches 1416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		/or /mo /db	- F 5 8 5	AUTHORS Barbet, A.F., Whitmire Moreland, A.L., Mwangi TITLE Ehrlichia ruminantium methods of use	M Ehrlichia ruminantium Bacteria, Proteobacteria, Alphaproteobacter Anaplasmataceae, Ehrlichia.	GI:29371591		4741 CTAATTGATC 475	4681 CAGAACTTACATATTCATTACCATCAATATTTTATCAACAGTAAATCCACAAATTGA 4	4621 TCARATCAGCCARAGGCACAAAAAGATGACCTTGCATCAACAAGTTACGTATTCAT 468	4561 GTAACAGCCAAAACGCACAAAAAAAGATAGACCTTGCATCAACCAAGTTTTCATTCA	Db 4501 TATCATGATACCAATTTGCAAAAGCAGAATATTCTTGAACTGTTATCTTAAAGTATTTG 4560 OV 4561 GTAACAGCCTCTTAACTGAGGCATTTTTGATCCATGGATGACTGATAGACTCTATTTTGTTC 4600	Db 4441 CCCGTATATTACAATTATCAACAATAATATGTCCAAAAACTATCAATGATAGAATTTTTGT 4500 QY 4501 TATCATGATACCAATTTGCAAAAGCAGAATATTCTTGAACTGTTATCTGTAAAGTATTTG 4560
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7 3787 AICTTTTATTAGATTTCTGATCAACTTCATCATCAACAACTAATACTTCAGAAATATATA 3846	7 3727 CTTGATCGCGGATAAACCATCAACTGCTAATTTAGTGACATAATTATCATCACTTAATAT 3786	1201 ATCAGATCCTCTTAACCATATATCCAATAATACAATCAGGCTCTTTTTCATAAGCCAT	1141	3547 ATAAGGACCGATATGGAGAGACTTTACAGGAGTGGGAATATTACGATGCCGACTAATGAT	Y 3487 TATAGCTCTCTTTACAACTAACTTTAATCTTCCTTCTGTAAAAGGCTTTTCTATATAATC 3546	9 3427 TICATAATCCTCAAATGCTGATTTCAACTCATCATTTTCTCTACGTAATCTACCAGACTC 3486	Y 3367 AGTAGCTGCTTTATTAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTAT 3426	y 3307 CCTAGCAACTACTTCCTTCCCAACACCTGGCGAACCAGTAATGAGTATACGACTCGATGT 3366	y 3247 CATAGATGAGTACATAGATATAAATGGAGTATCATACCCCTTGGATTTTTTATGTATTAG 3306 	Y 3187 CAATATATTACTTCCTCACTACCAAATATATTAACCAAGTAATTATTAGCTGGTAG 3246 	Y 3127 AAATAACGTACCATGATTTGCTTGCTCTATAATTCCAATATGAGAGGTACTCTATGAGA 3186	y 3067 CIGTAATAATCIGAGTAATCTTAATTGCGTATCGTTACCTGTAAATCTGTTACTTCATCTAT 3126	Y 3007 AATAATTCTCACATCTATACTAACAGGAATCTTACTATTTTTCCCTATATATTTTTCCCTC 3066	Y 2947 TAAATCCTCACAAAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGAAGAACAC 3006	Y 2887 ATCTGTACAATATTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATA 2946 	Y 2827 AGTACACAAACCTATTTTTTTACAGAIGCTATTCATAAATACCTACACAATTCCGGTAT 2886 	Y 2767 TAAGTTACCTGGCCATTCATATGACTGCCATTGATAAGCTTCATCACTTAATACATG 2826	

Query Match Best Local Similarity 100.0%; Pred. No. 4.4e-115; Matches 984; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 984; Conservative 0, Mismatches 0; Indels	RESULT 4 AX685247 AX685247 AX685247 DEFINITION Sequence 54 from Patent WO02066652. ACCESSION AX685247 AX685247 AX685247 DEFINITION Sequence 54 from Patent WO02066652. ACCESSION AX685247 AX685247 AX685247.1 GI.29371589 ENTICHAIR runninantium Bacteria, Proteobacteria; Alphaproteobacteria; Rickettsial) Barbet, A.F., Whitmire, H.M., Kamper, S.M., Simbi, B.H., Ganta, R.R., ANDHORS ANDRORS ANDRORS	Db 1321 ATCTTTTAGATTTCTGATATCAACTTCATCATCAACTAATACTTCAGAAATATA 1380 Qy 3847 CAATCTTTCCTTGGACATTTCAAAATCCTGTGCCAT 3882
AX685250 AX685250 AX685250 DEFINITION Sequence 57 from Patent WO02066652. ACCESSION AX685250 VERSION AX685250 Ehrlichia ruminantium Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; ANDHORS ANDHORS Barbet,A.F., Whitmire,W.M., Kamper,S.M., Simbi,B.H., Ganta,R.R., MOTELE Moreland,A.L., Mwangi,D.M., Mcguire,T.C. and Mahan,S.M. Barlichia ruminantium polypeptides, antigens, polynucleotides, and methods of use Patent: WO 02066652-A 57 29-AUG-2002; UNIVERSITY OF FLORIDA (US) FEATURES SOURCE I. 597 Organism="Ehrlichia ruminantium" /mol_type="unabsigned DNA" /mote="Complement to SEQ ID N0:52, nucleotides 41544750 Hypothetical cell division protein ftsQ Product =	QY 1052 AAAGAATTGCAGAACATCTTCCTTGTAGTATAGTACTGCTGGTGATAATAAAAATTT111 Db 421 AAAGAATTGCAGAACATCTTCCTTGTAGTATAGTACTTCTGTGTGTATAAAAATTATTACATCAACAT 480 421 AAAGAATTGCAGAACATTGCAGAACATTAGTATAACTTCTTGTGTGTG	Db 301 ACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAA 360 992 ATAGCAGAAGAAATTTTACAATATAATCCAATTTTATACTCTCTGGTCCAAGTTTTGCT 1051

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                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                          AUTHORS
                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4694 TTCATTACCATCAATCAATATTTTATCAACAGTAAATCCACAATTGACTAATTGATC 4750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4574 PACTGAGGCATTTTTGATCCATGGATGACTAGACTCTATTTTGTTTCTCAAATCAGCCAA 4633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4514 ATTTGCAAAAGCAGAATATTCTTGAACTGTTATCTGTAAAGTATTTGGTAACAGCCTCTT 4573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4454 ATTATCAACAATAATATGTCCAAAACTATCAATGATAGAATTTTTGTTATCATGATACCA 451:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4394 ATCTAGATGAGGTTAACGCACCATCTCCATGTATTGAAGTCAAATCATCCCGTATATTACA 4453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4154 ТТАТТТСАТТАТАТТААССТТСССТБСБААСАСССАТСТСТАТАСТТТСССАТАСТААЛАЛ 4213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4334 TGTGATAGATGAAACCATACCACCAACAAGAGTATTATCATTGACTACTTCACGTATAAA 4393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4274 AGGTAATTTTATATTTAAACCACTAGACAAAATAATATCCCCACCAATGACTATCAACATA 4333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4214 CTCACTTGAAGCTTTATAGATATTCAATAATTCACGCCAAGCAGCATAAGAATCATTATT 4273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 AGGCACÁAAAAAGÁTÁGÁCCTTGCATCAACAAGTTTACGTATTCATCAGAACTTACATA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTCACTTGAAGCTTTATAGATATTCAATĀATTCACGCCAAGCAGTAAGĀĀTCATTĀTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTATTTCATTATTATTAACCTTCCCTGGAACACGCATGTCTATAGTTTTCCATACTAAAA
                                                                                                                                                                              Barbet,A.F., Whitmire,W.M., Kamper,S.M., Simbi,B.H., Ganta,R.R., Moreland,A.L., Mwangi,D.M., Mcguire,T.C. and Mahan,S.M. Ehrlichia ruminantium polypeptides, antigens, polynucleotides, and
                                                                                                                                                                                                                                                                           Ehrlichia ruminantium (heartwater rickettsia)
Ehrlichia ruminantium
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                            Patent: WO 02066652-A 53 29-AUG-2002; UNIVERSITY OF FLORIDA (US)
                                                                                                                                                                                                                                                                                                                                                           AX685246.1 GI:29371588
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53 from Patent WO02066652.
                                                                                                                                                                                                                                                                                                                                                                                                                   AX685246
                                                                                                                                                                                                                                                               Anaplasmataceae; Ehrlichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
              /mol_type="unassigned DNA"
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1. .371
/note="Complement to
                                                                  organism="Ehrlichia ruminantium"
                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                 371 bp
SEQ ID NO:52, nucleotides <1_371
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TITLE
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                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome.
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                                                                                                                                                                                                                                                                                                                                     Nature 396 (6707), 133-140 (1998)
                                                                                                                                                                                                                                                                                                                                                           mitochondria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTATTCGACAT
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63. .1046
                                                      /db_xref="taxon:782" 63. .1046
                                                                          .mol_type="seromic DNA"
/strain="Madrid E"
/db xref-"--
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                                                                                                                                                                  Location/Qualifiers
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61 GCTTGACTGTCTATATAGTACATACGTGATAGATAACGAAAAAAATTTCTCAAAGCAGAC 120
Direct Submission
Submitted (11-NOV-1998) S.G.E. Andersson,
Siv.AnderssonSmolbic.uu.se, Dept. of Molecular Biology, University
of Uppsala, Husargatan, 3, Uppsala, S-751 24, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia prowazekii
Rickettsia prowazekii
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
                                                                                                                                                                                                                                                                                                                                                                                                  Andersson, S.G., Zomorodipour, A., Andersson, J.O., Sicheritz-bonten, T., Alsmark, U.C., Podowski, R.M., Naslund, A.K., Eriksson, A.S., Winkler, H.H. and Kurland, C.G.
The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPXXO3 279110 by DNA linear BCT 02-SEP-
Rickettsia prowazekii strain Madrid E, complete genome; segment
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//db_xref="GJ:392064"
//db_xre
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/gene="RP483"
complement (3174...4463)
/gene="RP483"
/codon start=1
/transT_table=11
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complement(1316. .3091)
/gene="RP482"
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/gene="RP484"
/codon_start=1
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complement(4633. .4965)
/gene="RP484"
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VICIGTLNAWVLTSGQIALGLAEDGLLPKFFAKKNSNNAPTYGIIISCLGITPLLLFT
SNNNFAKQITQIIDFSVIAFLFVYLICSLAFLKVIFSSKENFSYYYLFVAIISIIFCT
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complement(1194..1265)
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complement(1194..1265)
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/db_xref="GOA:Q9ZD62"
/db_xref="SWISS-PROT:Q9ZD62"
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TIDEYQQIVKSKTAELFGAACEVGAIIAEQVDRVSKDVQNFGRLLGTIFQVIDDLLDY
LGSDKQVGKNIGDDFLEGKVTLPLIFLYHKLEQDKQLWLENWLKSDKRTKDDFVKIRD
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1065. .1138
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codon_start=
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                                                                                                                                                                                                      gene
                                                                                                                                             SdS
                                      /codon_start=1
/transl_table=11
                                                                                                          /gene="RP489"
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/transl_table=
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/transl_table=
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/translation="MITCHING TO DRIVKEYIISLMDKELNESSAHTSGRFAKNII ETARSQIATSLGITMSREYNIIFTSSGTESNNLIMKNFYDGDIFISAIEHLSIYNHIN YAPNIKIIRVNKQCLVDLEHLEDLLSQSNASKKLVSYMIANNENGVLQDIAAISKITK KYNAKEHSDLVQSFKKISLNIKEGLDFATISGHKIGGGHGCGALISNSRFQLIFJII GGGQEKSVRSGTENVLAIAGFGLAAEFRRKDISKNYIKIRYLQERLEQKLKEYSNVNIISNNVARLANTTLITUNTDAQVKLIGFDLRNICVSGSACGSGKISKSHVLTNMGIR EEEARSSIRISLSHTNTISDIKAFIKAFEEIYEYKSSCHHCI" COMplement (7931. .8125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="00A;Q9ZD60"
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/translation="MILKIKEIYTVWAILELATNISNGPIILDKVSIKHNISLNYLAQ
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complement (8277. .9143)
                                                                                                                                                                                                                                                                                                    /product="unknown"
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/db_xref="GI:3861041"
/db_xref="GOA.Q9ZD58"
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/gene="RP487"
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complement(5430...6662)
/gene="RP486"
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/gene="RP485"
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/EYADNKNQFDEVVEEKGVRILIDPKILMYILGSEMDYVEINFKSQFIFINPNEKANC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GOA:Q9ZD59"
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EVGDDEIITDAKFKTFGCGSAIASSSLVTEWIKGKSVEDAKEIKNTEIAKELSLPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     omplement (4969. .5364)
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Matches 1021; Conservative
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Best Local
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Local Similarity 53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110238 GAATCATATAAGGTTTTATAATTTĆATTATTACCTGTAGTTAACGGATTĆAŢĀĀŢŢĀĀĀG 110179
                                                                   109878 CGCAAGGTTTTGTA---ATAGTTTGATCTTTAAGGAATTTTAATAATTTTTACTTGGATAG 109822
                                                                                                                                                                                                                                                                                                                                                                                                                                       110058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2637 TAACTITAGCACTTAAAACATCATT-----AATAGGCGAATTAGATACTATATCTACTG 2690
         TACTATTTTCCCTATATATTTTTCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTAT 3098
                                                                                                                                                                                                                                                                                                                                                                   TAATTGGAAGGACATTTAATCTATAATATAAATCCTCACAAAACCTACCAGCTTTTACTT 2978
                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCATTCTATAACATTACGTAATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATTG 2798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAAATCTTTTGCTGTAATCATCTCCTTAGGA-----GATTTCATAATTAAAA 2738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGTGCTGATAGATATTGACGTTCAAAAACTTCTCTAGCTTCTCTAAGCGGCATAGATA 110299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      АСТGAGTTTTTAAATACTGTCTTTCAAATTCTTCACGAGCTTTACGTAATGGTACAGAAA 2636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTTATTCTATTTGTGGGCGGTATATGTAGGCTTAATATTTTAGTTTTCGATGTAAAG
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                                                                                                                                                                                        CATCTTGGATATTTTTAGCAGTACTGGTAATAATTTTTATATCAACTTTAGTCTTTTTTC 109879
                                                                                                                                                                                                                                              CACTTTCAATATCTTTGGAAGAAGACACAATAATTCTCACATCTATACTAACAGGAATCT 3038
                                                                                                                                                                                                                                                                                                         TTÄÄÄGÄÄÄÄÄÄCATTÄÄGGCGATAATATÄGATCTTCTAGAAATTTTCCGTTATTÄÄCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATAAAATACCTACACAATTCCGGTATATCTGTACAATATTCTACTAAAGACGGTACTC 2918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAATAGCTTCATCAGAAAAGTGACGTTCTTTAAACCTGAAAATTTTGAAAAGTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCATTCAACAACGTTACGTAATTGTCTAATATTACCAGGCCATTCGTATGATGAAGAG 110119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGATCTTTCCATACCGACAAATGAAGAAGTTTTTGAAATATTATTATTAAAAACGACTCA 110359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAACGTTCCATTCCAACAATTCAGCAGTTCGTGATACATTACCTCCAAAACGAGATA 2576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTACGGTGTAATG 2516
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SBIFKQNEVILTPEIIKKYFADNLLYAPNLFIFFGTÞVIILFWFVTFLLERSIIVLLV
YGLANLLTTKTISQTSIKLVMFSSGIPIILQPVIIILIPELSILIQLLQMFTTFLVFV
AILQINKSLSHI"
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/gene="RP490"
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/db_xref="SWISS-PROT:Q9ZD57"
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transl_table=11
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Pred. No. 5.9e-37;
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4175 CCC---TGGAACACGCATGTCTATAGTTTTCCATACTAAAAACTCACTTGAAGCTTTATA 4231
                                                                                                                                                       4115 ATCAACTTTGTAAACCTATAGTAACTAATTATTAATAATAATTATTTCATTATATTAACCTT 4174
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                                                                                             AGTGTGTTTGTGACATAAAATAATAAGAATACTGATAATTTTAGTGTTTTTAACTGGATT
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                                                                                                                                                                                                                     -----AGTGTTATAAATATAATGAATTATGTGGATACTGTAGTAGTCATTGTGTAACT 10882
                                                                                                                                                                                                                                                                               AAGCATAGGTTTCCTATATATCCAAAAAAGAAAAATAAAAACACTTAATAAAAAACTTATC
                                                                                                                                                                                                                                                                                                                                      TATTAGTTGTTTTATAAATCTATAAGATTTTAATTTTAAATTTGATTTGCAGTTTAT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCATCATCAACAACTAATACTTCAGAAATATACAATCTTTCCTTGGACATTTCAAAATCC 3874
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Selfish DNA and the origin of genes
Science 291 (5502), 252-253 (2001)
3 (bases 1 to 12477)
Ogata,H., Audic,S., Renesto-Audiffren,P., Fournier,P.-E., Barbe,V.,
Samson,D., Roux,V., Cossart,P., Weissenbach,J., Claverie,J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-APR-2001) Unite des Rickettsies, Faculte de Medecine, CORS UMR 6020, Universite de la Mediterranee, 27 boulevard Jean Moulin, Marseille Cedex 05 13385, France
A public version of R. conorii genome database is accessible at http://igs-server.cnrs-mrs.fr/. The database intends to provide updated data. Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful. Comments to the
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Ogata, H., Audic, S., Renesto-Audiffren, P., Fournier, P.-E., Barbe, V., Samson, D., Roux, V., Cossart, P., Weissenbach, J., Claverie, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mechanisms of evolution in Rickettsia conorii and R. prowazekii Science 293 (5537), 2093-2098 (2001)
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Selfish DNA in protein-coding genes of Rickettsia
Science 290 (5490), 347-350 (2000)
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Rickettsia conorii Malish 7, section 72 of 114 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  authors are appreciated
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                                                                                                                                                                                                                                             note="REP06, A and T rich repeated element"
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5281 . .5332
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TTIINVNFENSKFSHVLMSNNTIDGVNFQKANLQNNSFKNTNITNSIFYGTDLEKSII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (5684. .7465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5684. .7465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (5047. .5136)
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   IDHGGGGSKAAAPVARKIMSDVLDKYL"
                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: RC0852"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="RC0851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="REP02,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="RC0851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product = "unknown"
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Best Local Sin
Matches 793;
                                                                                                       Query Match
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       2437 TTCHTACATAAATAATTATACATGCAATGTTTATTCAGAAACATTACACAATCCAAGAAT 2496
                                                                                     Similarity
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YTFSNLLSHVVGYVGEDSVGLSGLELAYDKYLTNSDYELNEPKRKEFLQLSIDIRLQ
YTTSNLLSHVVGYVGEDSVGLSGLELAYDKYLTNSDYELNEPKRKEFLQLSIDIRLQ
                                                                                                                                                          complement (11029, .11952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="REP02, RS3-like repeat" complement(10447, 10472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SILSEEIDKTIKQFKAIGAVGIIADPNNGEILALVNKPDFDPHYPSLAKPEELFNIAS
LGIYEMGSVFKALTMAVGFDTGVINNADAVDISYMKVGGFQLKVDYTPRQCWHSVPEIF
LYSSNIGTSQJMLEIGKSNFKKYLKKLGLLDQLOIELPERGTPLPFBEKERNBLTSVI
MSYGYGISISPLHFVRAMLPVVNGGTLYDLTLLKRKDEKVIGTKVFSENTSTQMKKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (10325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIIFIRFDEPKPTKESFGFATASWTAAPTAGRVFERMISLYGLEPIEQSEEES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="synonym: RC0855"
complement(8595. .10280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="REP03, repeated element"
complement(8226, ,8420)
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                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                            complement (10624. .11022)
                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RC0856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (10624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="REP02, RS3-like repeat"
10511. .10634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10418. .1
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                                                                                                                                                                                                                                                                                                                                                                                 'gene="RC0856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="REP04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAL03392.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDSPMNYFKKYAK"
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                                                                                                                                                                                                                                                                                                                                    codon_start=1
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="pbpA2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="RC0854"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="unknown"
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                                                                                  55.7%;
                                                                                                          7.1%;
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                                                          0
                                                     Score 338.6; DB 1;
Pred. No. 4.5e-34;
); Mismatches 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeated element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .11022)
                                                     Indels 41; Gaps
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2899
                                                                               1078 CTATAACCTTTGATTTTAAATCTATATTTTCGCGTTTTTAACTTTGTTACTTCACAAGCTC
                                                                                                                                                                                                                                                                               1198 GTTCTTTACCGCTACCGACTTTACCGTGAATCATTATACGACAGCTAGAGGTAGCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2779
                                                                                                                                                                                                                                                                                                                                                                                                                              3259 CATAGAT-ATAAATGGAGTATCATACCCCTTGGATTTTTATGTATTAGCCTAGCAACTA 3317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3199 ACTITCCTCACTACCAAATATATTAACCAAGTAATTATTAGCTGGTAGCATAGATGAGTA 3258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1362 GTTATTGGCAAATTCTA------AGATAGTAGGGCGTTTATTATTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3139 ATGATTTGCTTGCTCTATAATTCCAATATGAGGAGGTACTCTATGAGACAATATATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3019 ATCTATACTAACAGGAATCTTACTATTTTCCCTATATATTTTTCCCTCCTCCTGTAATAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1539 GAATTTGCCATTATTAACTTCATCTTGGATATTTTTAGAAGTACCGGTGATAATTTTTAT 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2959 AAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGAAGACACAATAATTCTCAC 3018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2839 TATTTTTTACAGATGCTATTCATAAAATACCTACACAATTCCGGTATATCTGTACAATA 2898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1719 CCATTCATAGGATTGAAGAGCAGCGATAGTTTCATCGGCAAAGCTACGTTCTTTAAACC 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1779 TAACGGATTCATAATTAAAGTCCATTCAACAACGTTACGTAATTGTCTAATATTGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2671 ATTAGATACTATATCTACTGGTAAATCTTTTGCTGTAATCATCTCCTTAGGA----- 2722
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                                                                                                                                                                                                                               TATTAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTATTTCA----TAAT 3434
                                                                                                                                                                                                                                                                                                                                                                                 TGAAAATAATGAACGGATTATTAACCCTTTTAGATTGTTTATGAATTAATCTTGCTGCAA 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTTTCCAATTCGCCGAATAATTCTTGATTGATTTTTTCCGTAGTCATACAGGTAGGGC
                                                                                                                            CCTCAAATGCTGATTTCAACTCATCATTTTCTCTACGTAATCTACCAGACTCTATAGCTC 3494
                                                                                                                                                                                  TTGCTATTGCCATTTTATATTTTAAAGTTACCGAACATTCGCCTACTAATTCAGTTTTAT
                                                                                                                                                                                                                                                                                                                              CTTCCTTTCCAACACCTGGCGAACCAGTAATGAGTATACGACTCGATGTAGTAGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCAATTTTAATATTTTTTCCGCAAGGTTTTGTA---ATAGTTTGATCTTTAAGGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCATATAATGAAGGTACTTTTAGAGAGGATACATTAAAGGCGATAATATAGATCTTCTAG 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATTCATATGACTGCATTGCTATTAAAGCTTCATCACTTAATACATGAGTACACAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAAATTTTGAAAGTTGCTTAACAAAATACTTAACGAGTAGCGGTATATCTTCTTTTCT 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTTGCTAATATTTCAGAAGGTATCATATAAGGTTTTATAATTTCATTATTACCTGTAGT 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTCTAAGCGGCATAGATAACATATCAAAAGCTATCTTCAAGTTTTGTAAGATTAGCACT 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTATTATTAAAACGACTCATTTGTGCCGATAGATATTGACGCTCAAAAACTTCTCTAGC 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCAATTTACGGTGTAATGCTGAACGTTCCATTCCAACAAATTCAGCAGTTCGTGATAC 2556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTTCCTCATATTCTTCGTCATTTATTCTATTTGTAGGAGGTATATGTAAGCTTAATAA 2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATATAAATCCTCACA 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTACGTAATGGTACAGAAATAACTTTAGCACTTAAAACATCATT-----AATAGGCGA 2670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTACCTCCAAAACGAGATAACTGAGTTTTTAAATACTGTCTTTCAAATTCTTCACGAGC 2616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTAATTTACGATGCAAAGCCGATCTTTCCATACCGACAAATGAGGATGTTTTTGAAAT 1960
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SOURCE
ORGANISM
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AF176314
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ACCESSION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3675 CTCTTAACCATATATCCAATAATACAACATCAGGCTCTTTTTCATAAGCCATCTTGATCG 3734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3555 CCATATGCAGAGACTTTACAGCAGTGGCAATATTACCATGCCCACTAATCATAATAACAG 3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1018 TTGTAAGTAAATAACTAATTTATCATTATAAACGGTTTTTCTATATAATCGTAAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3615 GCAAATAAGGATACCTTTCTTTAAGCTTTTCCAGTACACTTAATCCATCAATATCAGATC 3674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee,H.J. and Kang,H.S.
Direct Submission
Submitted (07-AUG-1999) Microbiology, Seoul National University,
Submitted (07-AUG-1999) Microbiology, Seoul National University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zymomonas mobilis
Zymomonas mobilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zymomonas mobilis fosmid clone 42B11, complete sequence AF176314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sphingomonadaceae; Zymomonas
1 (bases 1 to 23906)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence analysis of 42B11 fosmid clone of Zymomonas mobilis ZM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF176314.1 GI:5834286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee, H.J. and Kang, H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGATTTCGTATACTCTCCTTCATCGTCTACTATTAAAACATC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGAGTACTATTAGCGGCAACCTTAGGGTTAAAACCTTCATCTTTCAAATTTGCAGCAA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGATAAACCATCAACTGCTAATTTAGTGACATAATTATCATCACTTAATATATCTTTTA 3794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Zymomonas mobilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="fosmid 42B11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 to 23906)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gltB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23906 bp
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Sg gene

CDS

complement (8759. .11065)

note="nitrogen regulation protein"

product="Ntry" codon_start=1

table=11

complement (8759.

.11065)

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SdC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="hypothetical protein; ORF1"
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Lahpeldtvovviladgigotlyogavgdrdlyopviggvprrdvinglkaaldrgykr
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QAFDLETVLAHQAWTGSDEPTDDAQVVRAFGKKIALVTGDRLLEKLTYPADESVAE
QMTEKNISVCGSGFDVIGFBAGDHIMLGGIKIPHDHGLAGHSDADVALHALTDALLGA
IADGDIGTHFPSDPQWKGANSTQFLEYAVALAKKAGAIIDHADVTVICEAPKVGPYR
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13873 14412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRYGSGLNYTEMIASQAMIRETROSLOKSTWDPYEEPISVOLVGCTPDDMAESAKLNO DRGAAIIDINGCEVRKVVGGDAGSALMRDLKLAASIIEATVKAVSLPYTLKORMGWD LNSLNAPELARIAQDIGVQMVTVHGRTRNOLYKGHADWAFVROVKDAVSIPVIVNGDI NSLDDAKTALQOSGADGIMVGRGSYGKEWLLSQLMQGLTDGEMEKAPSIDEQVRTITE HYDEMLSYYGTITGVNIARKHIGWYTKGLPASAEFRNKINREEDPDRVKRNAGRILPT
                                                                                                                                                                complement(15290. .15733)
                                                                                                                                                                                    PNEVVAEQKSFGDLGRSGIRLQAALCALSLLMPDASISQG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VADMGDAGKRAAIETMVSDIVSQKMKPQSCEIVNGFLPFVAEQPANKIGDVSVSTFAL
LKKIGKVGRILPFDICSGD"
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RQVGDLRRMVDEFSSFARMFKPVFRKEAISDIGRHALFLHEVAHPQIGFVFEAQEDLP
LMVCDQRQLGRALTNLVKNAVBAIEENDRGGSGHVMYTLKREDSHLIIEVADDGIGLP
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IAIYLAFVVAAVIVRPISHYMEAVRAIGSGDLCARTHLKHINDEIGTLGFAFNRMANK
LEECINTLMSVNYLLDSRAFTEAVLSGVSAGVLSVNSGVTIQLVNLSAVGKLIKADNK
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/db_xref="GI:5834296"
                                                                 /evidence=not_experimental
/transl_table=11
                                                                                                                                       /note="hypothetical protein; ORF5"
                                                                                                                                                                                                                                                                                                                                            product = "unknown"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein; ORF4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="unknown"
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/note="hypothetical protein; ORF2"
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PVTIESVAEKGIGNQEPAIPGLTRSRSE"
                                        product="unknown"
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/db_xref="GI:5834293"
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/db_xref="GI:5834292"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="nifR3"
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3374 GCTTTATTAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTATT---TCA 3430
                                                                                                    8224 GCGACCTCTTTCCCGACCCCAGCAGGCCCTGTTATAAGGACGCGGCTGCCCGTGCCTGCA 8283
                                                                                                                                                                3314 ACTACTTCCTTTCCAACACCTGGCGAACCAGTAATGAGTATACGACTCGATGTAGTAGCT 3373
                                                                                                                                                                                                                             8164 GCCGAAACGACAATAAAGGGCGCAGCGGCACGAGGACTCCACATATGGAGCAATCGGGCG
                                                                                                                                                                                                                                                                                     3254 GAGTACATAGATATAAATGGAGTATCATACCCCTTGGATTTTTTATGTATTAGCCTAGCA 3313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3134 GTACCATGATTTGCTTGCTCTATAATTCCAATATGAGGAGGTACTCTATGAGACAATATA 3193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7402 CCAAGGCTTTTTAACTTACGATGTAGAGCCGAGCGCTCCATACCAATAAAAGAAGCTGTT
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                                                                                                                                                                                                                                                                                                                                                     ACTCGTAAAATCTTGGCCTGTGTCGGAATGGGCATATCCGCGATTTCATCAAGAAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCACATCTATACTAACAGGAATCTTACTATTTTCCCTATATATTTTTCCCTCCTGTAAT 3073
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Pred. No. 1.3e-20;
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2 (bases 1 to 1421) Ren,S., Fu,G., Jiang,X., Zeng,R., Xiong,J Ding,Y., Jian,J., Tu,Y., Gu,W., Cai,Z., Sl Zhu,G., Wang,S., Shen,Y., Qiang,B., Chen Direct Submission Submitted (12-MAR-2002) Chinese National Shanghai, 250 Bi Bo Road, Shanghai 20120. Updated information will be available at (http://www.chgc.sh.cn/lep/). Comments to appreciated. Location/Qualifiers 1. 14211 /organism="Leptospira interrogal /mol_type="genomic DNA"	Bacterili Chase Ren, S.X Xiong, H. Xiong, H. Chu, W.Y. Chu, G.Y. Shen, G.Y. Shen, G.Y. Girons, J. and Zhac Unique I interrog Nature (ர மு ம	8644 3791 8704 3851	OY 3611 ACAGGCAAATAAGGATACCTTTCTTTAAGCTTTTCCAGTACACTAATCCAATAATCAATATCA	Db 8284 ACCCGTTTCAACGTAGCCCGCACGTGATTGATCGCACTGGAATTGCCAGACTCATTA Qy 3431 TAATCCTCAAATGCTGATTTCAACTCATCATTTTCTCTACGTAATCTACCAGACTCTATA Db 8344 GTATGCCCATTTTGGCCTTTAAAGAAGCGTTTTCCTGCCGCAATCTTTCGTTTCGTTTCGTTTCATATCATAA Qy 3491 GCTCTTTACAACTAACTTAATCTTCCTTTCTATAATGATCATAA Qy 3491 GCTCTTTTCGACAACTAATCTTACTTCCTTTCTATAATCATAAC Qy 3551 GCACCCATATGCAGAACAATAAGACGTTTCAAAGGGTTTTCTCAAAGCAATCAACG Qy 3551 GCACCCATATGCAGAGACTTTACAGCAGTGGCAATATTACCATGCCCCAAATCATATA AGACCCCATATGCAGAGACTTTACAGCCGTTGCAATATTGCCATGGCCGGAAATAACCAGC Qy 3554 GCACCCTTGTCGGATAGCCGGTTACAGCGTTCAATATTGCCATGGCCGGAAATAACCAGCAGCAGCAGCAGCAGCAGTACAACCAGCCAG
H., Lu,L., Lu,G., Jiang,H., heng,H., Yin,H., Zhang,Y., ,Z., Wen,Y., Xu,J. and Human Genome Center at 3, China our World Wide Web site othe authors are ns serovar lai str. 56601"	Xu,H., Zhang,Y.X., Y.F., Jiang,J.X., , Zhang,Y., , Zhang,Y., , Aang,Y., , Ma,W., Yao,Z.J., , Pa, Saint Chen,Z., Xu,J.G. Leptospira	linear BCT 28-APR-2003 6601 chromosome I, section	GARATATACCE 3/90 GARATATACAAT 3850 AGCGCCATTATT 8763		GGTTAATTCTTCA 8343 CCAGACTCTATA 3490 CTGGTTTCGGTT 8403 TCGGTTTCATAA 3550
CDS	gene	gene		gene	gene CDS

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PVEBAIRDGKFREDLYYRLNVIPITIPPLRERTSDIPLLVDYYISKTLEENNLLSKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (3112. .4458)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=
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/note="Replication factor Y"
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complement(328. .2271)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="56601"
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                                                                                                                                                                                                                                                                                                                                                                                  /gene="ntrX"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="I"
                                                                                                                                                                                                                                                                                                                                            locus_tag="LA2400"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEMKLNEKKVRKVLDQIHRLDPIGIGAKDVQETLLIQAKILKPEDLNLHILIRDHIKD
LEKLDYKSISKKMEIQLESVESLASEIKKLEPYPATLYTPNKPDYVIPDVIVREVDGE
FDIYINDEWIPRLKVNKEYKNILKNAKESDKEYIATKLSSAEWLIRSVNQRRQTLFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIGALIDSFNQMVKDLKSKDAELMQSQRIAAWKEVAQRMAHEIKNPLTPIQLSAERIR
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VVKLFEHTPKLKIATNISKGFPQLFLDQKIISRVFTNLLKNSIBAIERKREKEEIPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MNDETRYYLRDLLILGLILLSVVLAEAIQESDQKTIPDDISFL
DRIVVVIFFFIPLESISILISVEYRNKRNLETGRLKSSIRYRLTISFIFVAFLPSIPI
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ASYRPDYCMYFIRIPFPTGNYNLQTGIRIHKDSERNVYSVISTRRNYDRADLTKEKLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (6505. .7470)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKSIMGLMMLALAPGNEFKIQVEGEKEDEALEALSNIVNNDFV"
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QKSVIDHSGHISVDSSSMGGCSFQIELPVS"
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complement////
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                                                                                                                                                                                                                                                                                                                                  complement (7475. .8896)
                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (7475. .8896)
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                                                                                                                                                                                                                                                                                                                                                                                                         'gene="rpoN"
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                        3211 ACCAAATATATTAACCAAGTAATTATTAGCTGGTAGCATAGATGAGTACATAGATATAAA 3270
                                                                               3790 TTCGAATTTTCCGATTCTAGAATCGGTCGCGCCCG-----TAAAAGCTCCTTTTGTAAA 3843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2491 AAGAATTTTCAATTTACGGTGTAATGCTGAACGTTCCATTCCAACAAATTCAGCAGTTCG 2550
                                                                                                                                                                                                                                                                                                                                    3031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2851 GATGCTATTCATAAAATACCTACACAATTCCGGTATATCTGTACAATATTCTACTAAAGA 2910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3370 AATACAAAGCCTTTCCATTACATTTTTTAGTTCCCGAATGTTACCTGGCCAAAAATGATT 3429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3310 TTTAAAACCTTTGAGTGCGTCTTTGCGTCGTTTGCAGTAATCACGGAACCTACGGTCAT 3369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2671 ATTAGATACTATCTACTGGTAAATCTTTTGCTGTAATCATCTCCTTAGGAGATTTCAT 2730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3265 TTTAGCTTTTCTAAAATCTCCTAACTCCACCATTTCGTTTGCA------GT 3309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2611 ACGAGCTTTACGTAATGGTACAGAAATAACTTTAGCACTTAAAACATCATTAATAGGCGA 2670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3205 GGTCACGTTTCCCTCATTTGTTTGTAATGTTTTTATAATATACTGTCTTTCAAATTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2551 TGATACATTACCTCCAAAACGAGATAACTGAGTTTTTAAATACTGTCTTTCAAATTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3145 AAGCGACTTCATTTTTCTGTATAAGTGAGAÄCGTTCAATTCCTÄAAACTCGGGAÄGTTCT 3204
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                                                                                                                                CTCTATAATTCCAATATGAGGAGGTACTCTATGAGACAATATATTATTACTTCCTCACT 3210
                                                                                                                                                                                                                                                                                   CGTCTCTGTACTTCCCAATTTTTCAAATCTTTGCTCTTGAAGAATTCGTAATACTTTCGC 3729
                                                                                                                                                                                                                                                                                                                                  AGGAATCTTACTATTTCCCTATATATTTTTCCCTCCTGTAATAATCTGAGTAATCTTAA 3090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĠĠŤŦŦŤĠĠŖŖĂŤĂŦŔĀŤŔAŦĊĊŖĊŖĊŖĠŖŖŦĠĠŖŖŦŔŦĊĠĠŖŖĠŦŦĊŦŤĊŦĊŦŖŖĠŖĠ 3549
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                                                                                                                                                                                 CTGAGTAGAAAGTGACATGTCACAAATTTCGTCCAGAAACAAAGTGCCTCCGTTGGCGGC 3789
                                                                                                                                                                                                                               TTGCGTATCGTAAATCTGTTACTTCATCTATAAATAACGTACCATGATTTGCTTG 3150
                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTACTTCACTTTCAATATCTTTGGAAGAAGACACAATAATTCTCACATCTATACTAAC 3030
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GSTHDLVNDPETRRIYLGEDFTL"
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ILETMNLSRTEIIKRRDDLLIELQIMRVANQKGYTLSGGERRRCEIARALVTNPDFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (8893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Locus_tag="LA2406"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Locus_tag="LA2405"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11001)
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fiers fiers cachia endosymomic DNA"	AUTHORS 12386340 AUTHORS Nikoh,N. and Fukatsu,T. TITLE Direct Submission JOURNAL Submitted (28-FEB-2002) Naruo Nikoh, North Carolina States Univ., Genetics; Gardner Hall, Raleigh, North Carolina 27606, USA	ARFERENCE I AUTHORS Kondo, N., Nikoh, N., Ijichi, N., Shimada, M. and Fukatsu, T. TITLE Genome fragment of Wolbachia endosymbiont transferred to X chromosome of host insect JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14280-14285 (2002)	Wolbachia er Wolbachia er Bacteria; Pr Rickettsiace	AB080665/c LOCUS AB080665 11400 bp DNA linear BCT 02-NOV-2002 DEFINITION Wolbachia endosymbiont of Callosobruchus chinensis ORF1, czcR genes, pol, ftsz, BMEI0172, RP741, sdhB, pgpA, g3pdh pseudogene, complete and partial cds. ACCESSION AB080665 AB080665 AB080665 AB080665 AB080665 AB080665 AB080665 AB080665 AB080665 AB080665 AB080665 AB080665	QY 3811 AACTTCATCATCAACTAATACTT 3836 Db 4429 TGGTTCATCGTCTGCGATAAAATTT 4454 RESULT 11	QY .3751 TGCTAATTTAGTGACATAATTATCATCACTTAATATATCTTTTATTAGATTTCTGATATC 3810 Db 4369 GAAAGTTTCTACTTCGAAATTTTCGTCCTCTAAAATTTTCTTAAGAGATTTTCTGATTTC 4428	QY 3691 CAATAATACAACATCAGGCTCTTTTTCATAAGCCATCTTGATCGGCGGATAAACCATCAAC 3750	3631 TICTTIAAGCTITTCCAGTACACTTAATCCATCAATATCAGATCCTCTTAACCATATATC 369	Db 4135 ACTITITCGATCGAAGAGGTTTTCTAAAAAATCCAACAGCTCTTTTTTGTAGCAGC 4194 Oy 3571 TACAGCAAGTGGCAATAATACCATGCCCCACTAATCATAACAAGACAAATAAAAAAAA	QY 3451 CAACTCATCTTTCTCTACGTAATCTACGAGACTCTATGAGCTCTTTACAACTT 3510	Qy 3391 TCTCAAATTACGTATAACAGGGGAGTTACCGACTATTCATAATCCTCAAATGCTGATTT 3450	Qy 3331 ACCTGGCGAACCAGTAATGAGTATACGACTCGATGTAGCTGCTTTATTAATCATACT 3390	QY 3271 TGGAGTATCATACCCTTGGATTTTTATGTATTAGCCTAGCAACTACTTCCTTTCCAAC 3330 QI 3271 TGGAGTATCATACCCCTTGGATTTTTTATGTATTAGCCTAGCAACTACCTTCCTT	a a a Cartorotta a Chino a Cartorottura a Sociolituro in incare de la Cartorota a Cartorota a Cartorota a Carto
/ yerus / yerus / yerus / yeseudo / pseudo / pseudo / gene "pgpA" / yeseudo / codon_start=1	<pre>complement(83188731) /pseudo /codon_start=1 /transT_table=11 /product="putative acetyltransferase" gene</pre>	/gene="sdnB" /pseudo /codon start=1 /transT_table=11 /product="succinat	/transT_table=11 gene	gene complement (64896955) /gene="RP741" /pseudo CDS complement (64896955) /gene="RP741" /pseudo /Codon statt=1	CDS (597. 6495 6097. 6495 /gene="BMEI0172" /pseudo /codon start=1 /transl table=11	/codon start=1 /transl_table=11 /product="cell division protein ftsZ" gene 60976495 /Gene_"HWET0172"	CDS complement(48996097) /gene="fts2" /pseudo	TPNVTYSAAARSTTLIDQILPALKTIIQETINREVQÇLRFPVPQFTTAQRPRTSSLSL PTFPKPTDKCSSEKRKRESTATPGPSEEEAASSDDSATKSTKKKGWPKGKPRK" complement(48996097) /gene="ftsz"	/ dd_xrel="G1:244.05008" / translation="W4.75008" / translation="W4.75008" KNKBGDFKNVSPFLISRTMYGLIGDVKKISKTNDGILVETSSSKQAQRLMQIQYFAQF FVEVVAHPTLMISKGVITGSDLLNCNIEBILCHEGSSIGVIEVRRIKSKEDGNIVDTAN HILTFNKPTLPKEIKVAMYNLKVRPYIFSPLACFNCQKFGHTTTRCSFQKICVCGKQP HEGTPFOLSFULGNICGNHPAQSKÇCIKYKBEFAIQQIKTGNYTSYVEAKKNVAVQYF	<pre>complement(30494212) /gene="URF1" /codon start=1 /transI_table=11 /protein_id="BAC22720.1" /protein_id="BAC22720.1"</pre>	/ Jodon start=1 / codon start=1 / trans table=11 / trans (10494212) gene complement (30494212) / gene="ORF1"	/ yeardo / pseudo CDS / complement(12857) / gene="pol"	/strain="wBTuAus" /specific_host="adzuki bean beetle, Callosobruchus chinensis strain jC" /db_xref="taxon:188349" gene complement[12857)	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\

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Matches 664;
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                                                                                                                                                                AATCTGAAAAAAGATGTAGCAATAATTTTAGCTTGTAAGGGAATAGAAAAGTCTACATTA 1019;
                                                                                                                                                                                                                   CATATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTC 976
                                                           AAATTACCTAGTGAAATÁGTAAATGAAGTTTTACCTAACAATCCTATTGCTATTTTTCA 10137
                                                                                                                                                                                                                                                                      ATCCTCGCTGTTCCCACTCAATCTCTGAGGGAGGTATGTCAGCAATT---GCATAATTGT 10257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGAATCAATCAACGGGAAAAGAGAAAGTGACA---AGCTACCCGGTTGTCGAATTACT 10368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTACACATATAAACACTTACCGAAAAAATTTAAAATATTTACCCACATATCATCTACCA 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAATTTCACTCAGTA---GTGAGAAAGATGTGATTTTGTGGACTCGCAATGAAACTACA 10425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTAGCAAGAACTACAAATATAATGAGACACTTAACTTTAATATATTTCAAATTTAT 496
                                                                                               AAATTTCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTATACTCTCT 1036
                                                                                                                                                                                                                                                                                                                         ATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACAG 916
                                                                                                                                                                                                                                                                                                                                                                            GATAATGTGTCAGTAAAATTGGCTATTGGAGACACAAT----TAATGCTCCAGTAACA 10314
                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATT 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAAT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCAGGAATATTGTGTGGCAATATCAATTTTAGGTGCTGGTGCATGGGGTACAGCAATC 10482
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52.0%;
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Pred. No. 1.3e-18;
Pred. No. 1.3e-18; Indels 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6 from Patent W00200932. AX344555
                                                                                                                                                                                                                                                                                                                                                                         Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosis of known genetic parameters within the Patent: WO 0200932-A 6 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           artificial sequences.
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/noTe="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 < 223>-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 follows.-seq 03 00.001 yd.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.49.980-seq 08 2.100.001 1.849.980-seq 07 1.800.001 2.149.980-seq 10 2.700.001 2.449.980-seq 07 3.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.049.980-seq 13 3.600.001 3.673.778 <223>-Original length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piepenbrock, C. and Berlin, K.
                                                                                                                                                                                                                                          /mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                                            CTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAA-----
                                                                                                                                                                                                                                        CAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTAT 858
                                                                                                                                                                                                                                                                                                                         TACACATATAAAACACTTACCGAAAAAATTTTAAAATATTTACCCACATATCATCTACCAGA 798
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0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16
600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.(
1.549.980-seq 19 1.500.001 18.49.980-seq 20 1.800.001
2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001
2.749.980-seq 23 2.700.001 3.049.980-seq 22 2.400.001
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3.673.778"
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                   213914 TATATÁTAATÁTATATAAAATÁTATÁTAÁTAÁTATATATAAAATATATATATAAAATATATATA
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                                                      2046 TTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCATTAGTTCTTAATAAAATTGCT 2105
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                                                                                                                                                                                                                                                          TATTTATAAAATAATATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACATAA 1925
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                                                                                                                                                                                                                                                                                                                                                                               ACATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACAAATTCCTAT 1805
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REMARK
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                                                                                                                                                                                                                                                     Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                             Hattori, M. and Aksoy, S.

Genome sequence of the endocellular obligate symbiont of tsetse flies, Wigglesworthia glossinidia
Online Publication
ncurrent/full/ng986.html
                             Nature Genetics 3 September 2002: doi:10.1038/ng986; ;
http://www.nature.com/cgi-taf/DynaPage.taf?file=/ng/journal/vaop/
                                                                                                                                                                                                                                                                                                                                                                                Wigglesworthia brevipalpis DNA, complete genome, section 2/2. AB063522 BA000021
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School of Science; Kitasato 1-15-1, Sagamihara, Kanagawa 228-
Japan (E-mail:hattori@genome.sci.kitasato-u.ac.jp,
Tel:81-42-778-9926, Fax:81-42-778-9926)
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                                /protein_id="BAC24445;1"
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GDVMLNVKNOKVAPPQISAEILKKMKKTAEDYIGKSITEAVITVPAYFNDTORQATKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKKFFICKSKFFKNPTFSGLLLILFCFLAIFISNTNFWKTYNYI
INYPLIKINTHDKNFSLTNI'UNDILMTFFFLEIGIEIKHEMLYGSLKNKSRAILPGIA
AIGGMIFPALIYNFITKEDSISSGWAITVATDIAFAVGVLKILGHSIPHSLLIFLE
LAIFDDIGAILITAFFYSNHIDQYMILLSTLVILTILSINVLRVTCIY'YIFIFOILLW
ESIFLSGIHSTISGVILGILMPHSSYLSSSKYEKSMAFLKKSLSFLNKYFILPIFAFF
NSGINFSNFENLSSSLLPFGIFFGLVLGKPIGVFLFSYLSVKFKLSKLPVGISFKEIA
                                                                                                                                                                                                                                                                                                                                  DIEVPALDGRYKLRIPAETQTGRLFRMRGKGVKSIRSGHQGDLLCRVVVETFVRLSEK
QKSLLKELGISFVGRTGMYNSPRSKSFFDGVKKFFDGLTN"
                                                                                                                                                                                                                                                                                                                                                                                NNRRKRSNRGSDLQYNINLSLEEAVKGISKEITIPKLERCNICSGKGMQPGTSAQNCS
TCNGQGQIQMRQGFFSVQQTCPSCRGKCKIIRFPCRNCSGQGRVERSKNISIRIPAGV
DNGDKIRLSGEGEAGKLGGSSGDLYVKISVKEHPIFKREEHNLYCEVPINFAMAALGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MAKSDYYDILGISKNASDREIKTAYKRLAVKEHPDRNPGNLEAE
SKFXEIKEAYEVLLDPKKRAAYNQYGHTAFPOGSSNTEFTSNADFSDIFGDVFGDIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1675. .2799)
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        AGKIAGLDVKRIINEPTAAALAYGLDKKTGNRIIAVYDLGGGTFDISIIEIDDVDGEK
                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                        complement (2874. .4811)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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/db_xref="GI:25166253"
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                                                                                                                                                                                                          'note="Protein fate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/specific_host="Glossina brevipalpis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Protein fate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <sup>1</sup>LCGIGFTMSIFISNLAFQNINEKIIYIAKFSILISSIVSSVIGFLFLYFLYKKI
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KFGKFHGNDINTIKTSNNLVRLPLFFNLKNKDQKYIISNIYNFIDKYS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="wecE"
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GTNIKLSIENKDKENLTCQIKKFDKESPNYTKFNF1DFKYYKKNIF1YIKKIKID
IESKSLKDEIIKIFKKESDLKMTSISNFIKYKINSKLEYHGGFVELTDIKENMFVILK
FFGGCNGCSMAKYTLKEGIEKEIKKNFPNIKGVIDITDHIHSESSFY"
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LSSVHQTDVNLPYITADSSGPKHMNIKYTRAKLESLVEELIYKFLEPVETISLKDAKLK
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VLLLDVTPLSLGIETWGGVMTTLISKNTTIFTKHSQIFSTAEDNQSAVTIHVLQGERK
RSIDNKSLGQFNLDGIAPAMRGMPQIEVTFDIDADGILHVSAKDKNSGREQKITIKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="arg-CCG"
complement (7960.
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EIEKCINELELSIKGEDKKDIEIKIQSLIQISSCLVDFSKNKENLNKEDIIKTNKKEN
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                                                                                                                                                                              complement (9418. .10677)
                                                                                                                                                                                                                         complement (9418. .10677)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MVKKHKFYTKEDLLCSSRGELFGKYGPQLPAPNMLMIDRLVKVT
ENGGNYNKGFIKAELDINPNMWFFSCHFIGDPVMPGCLGLDAMWQLVGFYLGWLGGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNKTNDDVVDAEFEEIKDKKN"
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="arg-CCG"
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/db_xref="GI:25166256"
                                                                                                       codon_start=1
                                                                                                                                      'note="Transcription"
                                                                                                                                                         gene="rho"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Cell envelope"
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|db_xref="GI:25166257"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Fatty acid and phospholipid metabolism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .ement(7084. .7707)
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                       275714 TTTAAAAAAAGCTATAAAATATAGCAATAC---TATTGTAATAGCTGTTCCTAGTATAGG 275658
                                                                                                                 275774 TTGCAATAAAAATTTTTACCAAAAATAAATTTTCCTAATGATTTAAAAAATAGAAATTTC 275715
                                                                                                                                                         760 ААААААТТТААААТАТТТАСССАСАТАТСАТСТАССАGACAACATATATGCAACCAGCAA 819
                                                                  TATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACAACA 879
                                                                                                                                                                                                                                              TATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCG 759
                                                                                                                                                                                                      TÄGAAAÄGTGTTTTTÄTGGGGTAGAAÄTAÄAÄAAÄCÄTATGCAATCTCTTAAAAAAGATCG
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275950 AATAAATA----CTAATTAGTACATAAGAAAAGGTAATATATTTTGAGTAATTTCTCAAT 275895
                                                                                                                                                                                                                                                                                       276130 ATTTGATTATATTTTTAAAAAAAAATATATAATATTAATTAAATTTAAACAATTTTTAA 276071
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                                                                                                                                                                                                                 580 AATAAATAATATATAATTTTTGACTGGTTTCTTGATATAAATTAAGGTAAAAAATGAAAAT 639
                                                                                                                                                                                                                                                                                                                                                         520 TAATATCACATCTGACATGATTAACAATAGTAACACATTTCTTAACACTAGATAATATAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 ATAGTACTATCTAATTAATAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATA 459
                                                                     CAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGG 699
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NFVIKNEKKYVIVASHLGNPIEEKYDVNFSLTHIVNHKKKIIKVBIRLIQNYLNGFEA
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AKSIIGGGETVLAMRMFNFIDRFSYISTGGGAFLSFIEKQELPVLSELKKFKKYTNFK
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VLDILAPIGRORGLIVAPPKAGKTMLLOUIQGIS YMHPDCYLIVLLIDERPESYTE
MORLYKGEVIJASTPDEPSSRHVOVESMVIEKAKRLVEHKKUVIILLIDSITRLARAYNT
VVPASGKVLTGGVDANALHRPKRFFGAARNMEEGGSLTIIATALIDTGSKMDEVIYEE
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/protein_id="BAC24451.1"
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/db_xref="GI:25166260"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Energy metabolism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.3%; Score 204; DB 1; Length 349174;
47.8%; Pred. No. 1.3e-17;
ative 0; Mismatches 880; Indels 26;
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                                                                                       274649 ATTATTTGATATTTATTAATTTTAAATTTAAATAATATTTTTAATTÄCTATTAGTTAAC 274590
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                                                                                                                                                                                                                                                                                                                                                          1835 GATTATAAATAAGTCAAATTAAACTTTTTACTTATAAAATAATAATATGTTTGCACACTT 1894
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TTTCACTACATCATGTATATGAACATAATT--TTACATAAAATAACTAATAAAAGA 1952
                                                                                                                                                                                                                                                                       AGCAAAATTTTATTAAAATCTTTATTTAATTAATTAAAATTAATTÄTTTATTAATATATTT 274650
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTAGTTTACCTTAAAAATATTTAAATTTTATATTATATTTCATTATCTTTAATGAT 274770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAAAAATTGAATATATTAATAAAATATAATTTATATTGTAGTTTTTACTTTTTTTAT 274830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAĀGGĀTACĀATĀATAĪTĀĀĀGAGATTTTĀATTTĀTČĀTGTĀĀĀCACĀĀĀATĀĀĀCAT 275010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGT 1476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGATATCTTAGGAAGAGAACATGTTTGTCAATTATATCAGGACCATCTTTTGCAAGATA 275484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCTAGCTAATTATATAAACAAATTCCTATCTCTATCTCAATTAACCAATTGTTATCA 1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTTAACATCCAACTAAGTATGTAACATATTACATAACAAACTTAAGTATAACTTAAAAT 1774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACT 1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2013 CTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTT 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.vulgaris genes glnA, ntrB and ntrC. X68129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steglitz-Morsdorf,U., Morsdorf,G. and Kaltwasser,H. Cloning, heterologous expression, and sequencing of the Proteus vulgaris glnAntrBC operon and implications of nitrogen control on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glnA gene; glutamate-ammonia ligase; nitrogen regulator;
ntrC gene; two-component regulatory system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteus vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-AUG-1992) G. Moersdorf, Universitaet Bayreuth,
Lehrstuhl f. Mikrobiologie, Universitaets str.30, 8580 Bayreuth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEMS Microbiol. Lett. 106 (2), 157-164 (1993)
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                                           KNGTNLFAGDKYGGLSEMALYY I GGI I KHARALNAFTNPTTNSYKRLVPGFEAPVMLA
YSARNRSASIR I PVVASMKARR I EVRFPDPLANPYLAFAAQLMAGLDGI TNKI HPGDA
MDKNLYDLFPEBAKE I PTVAGSLEEALNALDADREFLTHGGVFTNDS I DAYLALLRTD
                                                                                                                                                                                   /db xref="SWISS-PROT: P28786"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene='
                                                                                                                                          RDPRSISKRAEDYLKSSGIADTVLFGPEPEFFLFDDIRFKNDISGASYAINDIEAAWN
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                         VQRVRMAPHPLEFEMYYSA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="glnA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Proteus vulgaris"
/mol_type="genomic DNA"
/strain="DSM 30118"
                                                                                                                                                                                                                                                                                                                                                          /transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160
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                                                                                                                                                                                                                                                              /db_xref="GOA: P28786"
                                                                                                                                                                                                                                                                                        /product="glutamate--ammonia ligase"
/protein_id="CAA48234.1"
/db_xref="GI:45900"
                                                                                                                                                                                                                                                                                                                                                                                    /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="-24/-12 signal"
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Local Similarity 49.6%;
                                                                                                                                                                                                                                                                                                                                                    2879 TCCGGTATATCTGTACAATATTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAAT 2938
                                                                                                                                                                                                                                                                                                                                                                                                               3932 AGAGATTTGGTTTCAACACCCAGCTCTTTTGCCGTTTTTTGCAGAAAGTAGCGCGCTAAA 3873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2699 TTTGCTGTAATCATCTCCTTAGGAGATTTCATAAATTAAAATCCATTCTATAACATTACGT 2758
                                                           GTTGCTGCAATAATTCGGACATCCACTTTAACAGGGGCATAGCCTCCAACTCGATAAAAT 3693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATTGCTATTAAAGCTTCATCACTT 2818
TTTCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTATCGTATCGTAAATCTGTTACT 3118
                                                                                                              GAAGACACAATAATTCTCACATCTATACTAACAGGAATCTTACTATTTTCCCTATATATT 3058
                                                                                                                                                                             CGATGGTAGAGATCTTCACGAAAATCGCCTTCATTCACTCGTTTTTCTAAATCCTGATGG 3753
                                                                                                                                                                                                                                     CTATAATATAAATCCTCACAAAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAA 2998
                                                                                                                                                                                                                                                                                              CTAGGAATATCTTCTGTTCTATCGCGAAGAGGTGGTAATTGGATACGAATCACATTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATACATGAGTACACAAACCTATTTTTTACAGATGCTATTCATAAAATACCTACACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTGTGGCATGATTTCTTGGCTTGCAGTCATAACCGTCAGCCAACGACACACATTTTCG 3993
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/transl_table=11
/product="NR II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGASQVRQGRFEQANGGSLFLDEIGDMPLDIQTRLLRVLAEGQFYRVGGYAFVKVDVR
I IAATHQDLEKRVNEGDFREDLYHRLMVIRIQLEPKIEDBRTEDI SSLARYEIQKTAKEL
GVETKSLHEGSLKTMMESYWGSGNYGLENVCRKLTVMTASQEIWPQDLFSEIRLADES
RKNINRLTSQHWSQHLSLWADEALGEGKENILNDALPQFERTLLLSALAYTQGHKQDA
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PKPFDIDETLALIERAITHYREQKQPNNAENILQSVSDMIGEAPAMQEVYRIIGRLSR
SSISVLINGESGTGKELVAHALHRHSPRALAPFIALNMAAIPKDLIESELFGHEKGAF
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/protein_id="CAA48236.1"
/db_xref="GI:45902"
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/db_xref="SWISS-PROT: P28788"
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/db_xref="GI:45901"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3656 AATCCATCAATATCAGATCCTCTTAACCATATATCCAATAATACAACATCAGGCTCTTTT 3715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3536 TCTATATAATCATAAGCACCCATATGCAGAGACTTTACAGCAGTGGCAATATTACCATGC 3595
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                  Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, B. Lewin, A., Lipscher, B., Maier, S., Model, F., Mueller, V., Otto, T., Pelet, C. and Ziebarth, H.

Methods and nucleic acids for the analysis of hematopoietic cell
                                                                                                                                                                                                                                        synthetic construct
                                                                                                                                                                                                                                                                                                                                                       Sequence 386 from Patent WO02077272. AX599046
proliferative disorders
                                                                                                                                                                                                      artificial sequences.
                                                                                                                                                                                                                                                                  synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.9%;
Best Local Similarity 43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1900;
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3826 АЛЛАСАЙЙАНТТСАЛСАЛАТАТТАЛАЛАСАТТАЛТТАТТАЛАТАСАТТТТСАЛАЙПААТА 3767
                                       1144 TGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAA 1203
                                                                                                                                                                                               1024 TTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTTGCAGAACATCTTCCTTGTAGTAT 1083
                                                                                                                      1084 AGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGA 1143
                                                                                                                                                                3939 AAATTATATTTTTTATCATTATTTTTCACAATTTTTTAAAAA.-----CATTAAAATCA 3887
                                                                                                                                                                                                                                             3999 TTÍAÁACATTTTTCÁTTÍTTTTTTTÁÁÁTÁACÁTÁÁAÁTTTÍATÁTTTTÁAÁTTTTÁÁÍ 3940
                                                                                                                                                                                                                                                                                                                                                                                                                4107 АЛАЛАЛАТТАСЛАТАТСЛАСЛАЛАЛАТЛАЛАЛАСАТТТАЛАЛАСЛОЛАЛТАЛАЛАТАЛТС 4048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4167 БАБАЛТАТТБАЛСАЛАЛАТАТТАЛААЛАТБАЛЬАСБАЛЬАССАЛТАЛАЛАЛАЛАЛАЛТТ 4108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4347 AAATAATTTCAAAAAATATCATAACAAATTTTTTAACATAATTATATTTTCATATTAA 4288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4465 CATATTTAATTTTTATTTTTATCACAATCAT--TTTCAAAATATTTTCACATTCAAAAT 4408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 964 AATTACATCACTCAAATTTCCCAGTGAAATAGCAGAAGTTTTACAATATAATCCAAT 1023
                                                                                                                                                                                                                                                                                                                                                                      904 ACAACACAAACAGCATATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGA 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                     844 CAATACATGTATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAAT 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     668 ACAGCAATAGCAATTGCACTGTCAGCACATGCTATATCAGTTAACTTATGGGGACGTGAT 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 CA----TAGAAATATTACACATATAAAACACTTACCGAAAAAATTTAAAATATTTACCCAC 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 TCTTCTTTGTTCCATCCATATTTTCCAATTATTTACAATATCATAGAGTTCTTTATTCG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 CAAATTTATTATACTACTCATCATATTTAGCATAATATCACATCTGACATGATTAACAAT 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 02077272-A 386 03-OCT-2002; Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                              ATAACAAAA-----AATTTCAACACAAAACAAAATTTACATAATCATTTCA 4000
                                                                                 ATTTCAATTTTTTTATCATTACAAAATCAATTTTCAAAATTTTACATTTCAAATTTTCAAA 3827
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/mol_type="unassigned DNA"
/db_xref="taxon;32630"
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1. .8056
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                     2817 ATAACAATTTTAATAÄACÄÄÄATTCATTTAAATTTATTAAAAAATAAACAATTAAATATTT
                                                                                                                                          2164 ACGTCAAATAAATTAAACAAATTTCTAATATAACCACCTACTCTAAACATAGGAACCAAT 2223
                                                                                                                                                                                  2104 СТРАТТАСССАЛАЛА GGTT ВАЛАТАСАСАТТССТ GCAACAAT AT GAAGAA GAT ACAATAC 2163
                                                                                                                                                                                                                                                                   1984 TATTTACTACGTAATATTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACAT 2043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1924 АЛГІТГАСАТАЛАЛТАЛСТАЛТАЛАЛАЛАСАЛАССАЛТАСАТАТАТТАЛАГТАСТАЛАЛАСАСС 1983
                                                                                                                                                                                                                                                                                                      2044 ATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCATTAGTTCTTAATAAAATTG
                                                                                                                                                                                                                                                                                                                                                2995 AATTTTTCAATAATTTTTTTTTTTTTTTTTAACAATAATTAATTCATTTAAATTTTACATT 2936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1864 CTTATTTATAAAATAATATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACAT 1923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1684 ССАСАТАТАТАЛАЛАЛАСИСТСАЛАТАСССАТССТТАЛСАТССАЛСТАЛСТАЛСТАЛСАТА 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1564 ATTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCAT 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1504 GATATCATTAGCAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTT 1563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1204 GAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAAATTTTAGGTAATAATGCTGT 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTTTTATTÄÄÄTTÄCÄCÄTAAAAÄTÄACAATAATTCÄAÄTTTCATTCÄCÄATTATAAC 3056
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mitochondrion Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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Direct Submission
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                                    1131 СААТААGТААТGATGTTCТАААААТААТАТАССАТСААGATATTATAGGTGTACAGATTG 1190
                                                                                                                                                                                                                                                   951 GTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATAGCAGAAGAAATTTTAC 1010
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                                                                        TCAATTAAATTÄTATAAATATAATAAAÄTAATTTÄTTTTAATCACTAAATCTGAAATAAT 1080
                                                                                                            TTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCATTGATAGAAA 1130
                                                                                                                                                                                                                                                                                                                        ТАТСТАСАСААЛТАСААСАСАААСАСАТАТСТСТАААААТАТТААТТТЭТА 950
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                                                                                4269 AAATAAAAATTTTÄAAÄTTTÄAAAATATATAGATÄTÄÄTTTATAAAAATTTATATTCTCAT 4328
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                                                                                                                                   CCAACAAGAGTATTATCATTGACTACTTCACGTATAAAATCTAGATGAGTTAACGCACCA 4415
                                                                                                                                                                                                                                             CTAGACAAAATAATATCCCACCAATGACTATCAACATATGTGATAGATGAAACCATACCA 4355
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Genetics 118 (4), 649-663 (
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Drosophila melanogaster and its subling species
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Clary, D.O., Wahleithner, J.A. and Wolstenholme, D.R.
Transfer RNA genes in Drosophila mitochondrial DNA: related 5'
flanking sequences and comparisons to mammalian mitochondrial tRNA
                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster mitochondrial DNA: gene organization and
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Drosophila melanogaster complete mitochondrial genome.
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Nucleic Acids Res. 10 (21), 6619-6637 (1982)
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1 (bases 12511 to 12682)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Lewis, D.L., Farr, C.L. and Kaguni, L.S.
Direct Submission
Submitted (03-OCT-1995) Laurie S. Kaguni, Biochemistry Department,
Michigan State University, East Lansing, MI 48824-1319, USA
Location Qualifiers
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Lewis, D.L., Farr, C.L. and Kaguni, L.S.
Drosophila melanogaster mitochondrial DNA: completion of the
nucleotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)
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Lewis, D.L., Farr, C.L., Farquhar, A.L. and Kaguni, L.S.
Lewis, D.L., corganization, and evolution of the A+T region of
Drosophila melanogaster mitochondrial DNA
MOL. Biol. Evol. 11 (3), 523-538 (1994)
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/product="tRNA-Gln"
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/db xref="taxon:7227"
/db xref="taxon:7227"
/note="derived from new and previously submitted
/note="derived from new and previously submitted
sequences; sequence is a composite containing sequences
obtained from different Drosophila melanogaster strains"
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/note="mechanism underlying reading frame shift after
first codon uncertain"
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/product="tRNA-Tyr"
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  293 TATTCAAAGAATACCTCTTCTCTTGTTCCATCCATATTTTCCAATTATTACAATATCAT 352
                                                Conservative
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TQGLFFTVLLGIYFTILQAYSYIEAPFTIADSIYGSTFFMATGFHGHHVLIGTTFLLV
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FIKWISSNNS"
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QWYWSYEYSDFNNIEFDSYMIPTNELWTDGFRLLDVDNRVYLFMNSQIRILVTAADVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="TAA stop codon is completed by the addition of 3' residues to the mRNA" \,
                                                                                                                                      6184. .6251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                               GLYHEWNQGMLNWSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLLRHLNNHFSKNHHFGFEAAAWYWHFVDVVWLFLYITIYWWGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "NAESSA
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/transl_table=5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="tRNA-Leu"
                                                                                                                                                            'product="tRNA-Asn"
                                                                                                                                                                                                                                                 'product="tRNA-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JTANMIAGHLLITLIGNTGSSMSYMLMTFILMAQIALLVLESAVAMIQSYVFAVLSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MPQMAPISWLLLFIIFSITFILFCSINYYSYMPNSPKSNELKNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="tRNA-Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="tRNA-Gly"
                                                                                                                                                                                                       product="tRNA-Arg"
                                           3.9%; Score 184; DB 3; Length 19517;
43.0%; Pred. No. 1.2e-14;
ative 0; Mismatches 2365; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5961
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16111 TTATTAAATTATACTTAATAAACTATTTTTATAAATTAATTATT	131 CARTAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGATTG 1190	15817 ATAAATAAATAAATAATAAATAATAAATAATTAATAATA	15642 TÁTÁTATÁTATÁTÁÁTÁCATATATÁTÁTÁTÁTATÁTATÁTAÁTAÁTAAÁTAAÁTA			15162 TATTAATAAATAAATTATAAATTTAAAATTTAAAATTTTAAATTTT
Db 17175 ATTATTTATAAATAATTAATAAATTAATAAAATTATATAT	2202 TACTCTAAACATAGGAACCAATAGTATATCATACCTAAGTATATACCTCAACATGT 17061TAAATTTATTCCCCCTATTCATAAATTTATTATATAAATTTAAAACTTAAAAAA	1684 TAATAAAATTTAAAATGATTTTTATAAAAATTCAATTCA	QY 1902 ACATCATGTATATAATGAACATAATTTTACATAAAATAAAT	1731 AGTATGTAACATATTACATAACATAAGTATAAGTATAACTTAAAATTTCCCTAG 16584 TATTTATATATATATATATATATATATATATATATATA	Qy 1551 CTAFTTACAATTATTACATGAGAATATATACACTAGATAAAGCCATAFCAACATATTAT 1610 Db 16404 TTATTATATATAAAACTTAAAAAAATTTTTTTTTAAAAAA	16231 1431 16291 1491

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3581 18415	3522 CTGTAAAAGGCTTTTCTATATAATCATAAGCACCCATATGCAGAGAGACTTTACAGCAGTGG
3521 18355	3462 TTTCTCTACGTAATCTACCAGACTCTATAGCTCTTTTACAACTACCTATATCTTCCTT
3461 18295	3402 GTATAACAGGGGAGTTACCGACTATTTCATAATCCTCAAATGCTGATTTCAACTCATCAT
3401 18242	3342 CAGTAATGAGTATACGACTCGATGTAGTAGCTTCTTATTAATCATACCTTCTCAAATTAC
3341 18182	3282 ACCCCTTGGAGTTTTTATGTATTAGCCTAGCAACTACTTCCTTTCCAACACCTGGCGAAC
3281 18122	3222 TAACCAAGTAATTATTAGCTGGTAGCATAGATGAGTACATAGATATAAATGGAGTATCAT
3221 18062	3162 CAATATGAGGAGGTACTCTATGAGACAATATATTATTACTTTCCTCACTACCAAATATAT
3161 18002	3102 ATCGTAAATCTGTTACTTCATCTATAAATAACGTACCATGATTAGCTTGCTCTATAATTC
3101 17942	3042 TATTITCCCTATATATITTTCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTATCGT
3041 17883	2982 TITCAATAICTITGGAAGAAGACAATAATICTCACATCTATACTAACAGGAATCTTAC
2981 17823	2922 TTGGAAGGACATTTAATCTATAATATAAATCCTCACAAAACCTACCAGCTTTTACTTCAC
2921 17763	2862 TAAAATACCTACACAATTCCGGTATATCTGTACAATATTCTACTAAAGACGGTACTCTAA
2861 177,03	2802 TTAAAGCTTCATCACTTAATACATGAGTACACAAACCTATTTTTTACAGATGCTATTCA
2801 17648	2742 ATTCTATAACATTACGTAATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATTGCTA
2741 17588	2682 TATCTACTGGTAAATCTTTTGGTGTAATCATCTCCTTAGGAGATTTCATAATTAAAATCC
2681 17528	2622 GTAATGGTACAGAAATAACTTTAGGACTTAAAACATCATTAATAGGCGAATTAGATACTA
2621 17468	2562 CICCAAAACGAGATAACIGAGITITTAAATACIGICTITCAAATICTICACGAGCTTTAC
2561 17408	2502 ATTTACGGTGTAATGCTGAACGTTCCATTCCAACAATTCAGCAGTTCGTGATACATTAC

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19365 AAATTATTTÄÄATAATTTTTCATÄÄAATTT 19394
                                                                                                                                                                                                                                19185 AAATAĀĀĀĀĀĀTTTTĀAAĀTTTĀAAĀATATĀGATĀTĀATTTATĀĀĀAATTTATĀTTCTCAT 19244
                                                                        19005 AAAAATTTTTAATAAATĀĀAĀTTTTATAATGAAATĀTTĀTTTATTTĀTTTTTCĀTTTTTT 19064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18836 TATATATTTATAAATTTATATATTATTGAATATTTATATATATATATATATATATATAGAA 18895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18896 AAATTAAATTATTTAAAT------AÄTTTAATATATAATÄTTTTTTÄÄAAATTTCTTÄ 1894:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18476 TCTTAAATGTATTATTTTATAAAAAATATTTATATAAAAAATCATGTTTTTTAAAAAA 18535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18416 ATÁTÁTATATÁTAGAAÁAATTAÁTTTÁTTTAÁATAÁTTTÁÁTATAAATTTTTAAATTTT
                                     4529 ATATTCTTGAACTGTTATCTGTAAAGTATT 4558
                                                                                                             4469 ATGTCCAAAACTATCAATGATAGAATTTTTGTTATCATGATACCAATTTGCAAAAGCAGA 4528
                                                                                                                                                                                      4416 TCTCCATGTATTGAAGTCAAATCATCCCGTATATTACAATTATCAACAATA-----AT 4468
                                                                                                                                                                                                                                                                     4356 CCAACAAGAGTATTATCATTGACTACTTCACGTATAAAATCTAGATGAGTTAACGCACCA 4415
                                                                                                                                                                                                                                                                                                                                                4296 CTAGACAAAATAATATCCCACCAATGACTATCAACATATGTGATAGATGAAACCATACCA 4355
                                                                                                                                                                                                                                                                                                                                                                                                                      4236 TTCAATAATTCACGCCAAGCAGCATAAGAATCATTATTATGGTAATTTTATATTTAAACCA 4295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4176 CCTGGAACACGCATGTCTATAGTTTTCCATACTAAAAACTCACTTGAAGCTTTATAGATA 4235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4116 TCAACTTTGTAAACCTATAGTAACTAATTATTAATAAATTATTTCATTATATTAACCTTC 4175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3936 ACACCTCATAATACTACCACACACACTAATGATCAACAACCAATATATTAAATTCATTAT 3995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3878 GCCATAATTACCTACAATACTAATGAAATACTGCAAACACAA--TGTACTCCTTTAAAGT 3935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3818 TCATCAACAACTAATACTTCAGAAATATACAATCTTTCCTTGGACATTTCAAAATCCTGT 3877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3758 TTAGTGACATAATTATCATCACTTAATATCTTTTATTAGATTTCTGATATCAACTTCA 3817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3698 ACAACATCAGGCTCTTTTTCATAAGCCATCTTGATCGCGGATAAACCATCAACTGCTAAT 3757
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ACU93899/C LOCUS AC093899 172816 bp DNA linear PRI 12-JUN-2002 DEFINITION Homo sapiens BAC clone RP11-724016 from 2, complete sequence.

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REFERENCE
AUTHORS
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            The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanses, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                      MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
MCPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JUN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Feb 5, 2002 this sequence version replaced gi:15625013.
                                                                                                                                                                                                                                SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Homo sapiens BAC clone RP11-724016 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MO 63108, USA
5 (bases 1 to 172816)
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Submitted (05-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restriction digest.
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Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC093899 AC068884
AC093899.3 GI:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://genome.wustl.edu/gsc
pBACe3.6
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NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-724016;
actual end is at base position 172816 of RP11-724016.
Unresolved simple sequence repeat from base position 22700 to
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25900.

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                                                    /rpt_fami
18177. .1
  /rpt_family="MER1_type"
19731. .20040
                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alu"
8360. .8551
                                                                          /rpt_family="Alu"
18025. .18110
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9136. .9174
                         /rpt_family="Alu"
19312. .19441
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2658. .2729
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chromosome="2"
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mol_type="genomic DNA"
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Matches 1219; Conservative
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                   478 TAATATATTTCAAATTTATTATACTACTCATCATATTTAGCATAATATCACATCTGACAT 537
                                                                                                                             418 ТААААААТССТСААТАСТСТТТАССААСААСТАСААТАТААТСАСАСАСТТААСТТАТ 477
                                                                                                                                                                                                    358 ГСТТТАТТССЯСАТАСАТАТТААААТСААТСАААСААААТААТААТААТТАСТАТТАА 417
                                                                                                                                                                                                                                                                           298 AAAGAATACCTCTTCTTCTTCCATCCATATTTTCCAATTATTTACAATATCATAGAGT 357
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30848. .30882
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27815. ,28151
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'rpt fac':
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21286. .21344
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20403. .20472
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25030. .25205
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3. .25398
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5. .24171
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4. .23977
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                                     24582 ATATTÁRATÁCRÁATGTÁTÁÁAÁTÁTAKATÁTATÁTATÁAÁTGTÁTAÁAACATRAATÁ 24523
                                                                                                            24697 TTTĀTĀTĀTĀĀĀCĀTĀTTĀĀATATCAĀ-----TĀTĀTĀTTTATĀTĀTĀĀTĀĀĀTATĀTTĀA 24643
                                                                                                                                                                                                                                                         24814 TAAAATATATCAAATATAAATATATATCAAATATAAATATATATTT---ATATGTAAA 24758
                                                                                                                                                                                                                                                                                                                                                                                                     24874 CAAATGTAAATATTAATATATATAAAAATATATATCAAATGTAAATATATTAATATATA 24819
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                                                                                                                                             1495 AAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCATATCTAT 1554
                                                                                                                                                                                                                    1435 TAGAAATATAAATAATTAATTAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGT 1494
                                                                                                                                                                                                                                                                                         1375 АТТААСАТСТАСААСАСААТСАСТСАСССААТАТСССТТТТССАСТАСААТАССАААТАССАТАС
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              2694 AATCTTTTGCTGTAATCATCTCCTTAGGAGATTTCATAATTAAAATCCATTCTATAACAT 2753
                                                                  2634 AAATAACTITAGCACTTAAAACATCATTAATAGGCGAATTAGATACTATATCTACTGGTA 2693
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Gardner, M. J., Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W., Carlcon, J.M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, I.T., Carig, A., Yames, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Craig, A., Kyes, S., Chan, M.S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Kyes, S., Chan, M.S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Angiuoli, S., Petera, M., Allen, J., Selengut, J., Haft, D., Anther, M.W., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Fraumholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and
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                                                                                                                                                                               Direct Submission
Submitted (02-OCT-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the human malaria parasite Plasmodium falciparum Nature 419, 498-511 (2002)
3 (bases 1 to 14867)
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Query Match 3.8%; Score 182.2; DB 3; Length 14867; Best Local Similarity 45.4%; Pred. No. 2.2e-14; Matches 1284; Conservative 0; Mismatches 1478; Indels 65;
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                                         1886 TGCACACTTTTTCACTACATCATCTATATAATGAACATAATTTTACATAAAATAACTAAT 1945
                                                                                                                             2066 AACTGTTTTTTTATGCCCATTAGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAA 2125
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                                         Clostridium tetani E88
                                                                                                          AEO15944 1 300205 bp DNA line Clostridium tetani E88, section 9 of 10 of the AE015944 AE015927 AE015944.1 GI:28204325
                       Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
    Clostridium
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Bruggemann, H., Baumer, S., Fricke, W.F., Wiezer, A., Liesegang, H., Decker, I., Herzberg, C., Martinez-Arias, R., Merkl, R., Henne, A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gottschalk, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology and Genetics, Georg-August University, isebachstr. 8, Goettingen 37077, Germany
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KDEILNVIKLIDSFYKVFGFEYFVELSTRPEDSMGSDEDWEVATNGLKVALEGAGLEY
KINEGDGAFYGPKIDFHLKDCIGRTWQCGTIQLDFQWPERFDLTYVGQDGEKHRPVMV
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complement(162. .683)
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                                                          /product="conserved protein"
/protein_id="AAO36766.1"
/db_xref="GI:28204328"
                                                                                                                                                                                                                                                             KLNYEIDNRIVENSK"
                                                                                                                                                                                                                                                                             VEFDDRNEKIGYKIREAQLQKVPYMIILGDKEVSENKVAVRSRKEGDLGAISLKEFVA
                                                                                                                                                                                                                                                                                                      HRVVFGSIERFIGILIEHFAGAFPTWLAPVQVKVMTITDSQKDYANKVVNDLKEKG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="threonyl-tRNA synthetase"
/protein_id="AAO36765.1"
/db_xref="GI:28204327"
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/db_xref="GI;28204326"
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="Massachusetts"
/sub_strain="E88"
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tag="CTC02287"
lent(3117
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/protuct="methyltransferase"
/protein_id="AAO36770.1"
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/translation="MECYKDFAQIYDNLIKEDVDYHSWSNFIMDIVNTHNVKKDNYLD
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PSHLTCCLDSINYLTSIEDVSSYFLRYVNHLKDEGIFIFDINSYYKITEVLGNNIYY
DSEEVFYTWENYLNKDIVENYLTFFIKKANSYYERFDEVHRERAYKMEWLEKLIKKNN
                                                                                                                                                                                                                                                                      complement (7879. .8619)
/locus_tag="CTC02292"
complement (7879. .8619)
/locus_tag="CTC02292"
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/locus_tag="CTC02291"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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AAALGRMLTAGSLMGSMLKSEKDTITIKIDGGGEAKGVLVTAYPEGKVKGYIGNPLVH
                                                                                                                                                                                                                                                                                                                                                                             QFCNEKYFYDHEKIGELLRIMNN"
                                                                                                                                                                                                                                                                                                                                                                                                             EEILEFIFEGMDLKILEGIVPEYTCDCSREKIDRALISIGYKDLKEIYDEGKTEELVC
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/protein_id="AAO36768.1"
/db_xref="GI:28204330"
                                                                                                                                                                                         /codon_start=1
/transl_table=
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PSAVGLGVLVDKDLSIKASGGFIIQMMPGADELLADFITYRLEEIPSITELISKGMSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (5403. .6491)
/locus_tag="CTC02290"
/EC_number="2.4.2.21"
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complement(5403. .6491)
/locus_tag="CTC02290"
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VTPIYLKKGKLIDRGSILCNE"
complement(5057, .5131)
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SGHPDILIHVLDEKNLILHKDIDKEFIKKLKNLNFNIKLSKNSLSSNYPMNIGLNAVN
LSNVFIHNLKYTDPVLIENVKDKNLINVKQGYTKCSVAVVSDNAIITSDKIIAQKAKE
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IDITEELFKDFISNNVSLEINLDDILISGLITYCPEKIIIHCVENCLNKELINTINNV
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note="codo"
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protein_id="AAO36767.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="codon recognized: UGC"
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                                                                                                                                                                                                                                               number="2.1.1.-"
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        45893 CTATCTÁÁAGCATCCCCÁGTTATTCCTTTTATATCTTTTTCTÁATTTTAATTTATACTTT 45952
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                                                         ATCCATTCTATAACATTACGTAATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATT 2797
                                                                                                            GCCCTTTCTATAATATTTTGTÄGTTCTCTAACATTTCCATGATATTTATATTTCTCAAGG 45892
                                                                                                                                                                                                                                                                                                                                                                          TTACGTAATGGTACAGAAATAACTTTAGCACTTAAAACATCATTAATAGGCGAATTAGAT 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCCATGGAAATGTTTTÁGATTATATTCTATAACCTTTTTTTTCTATGGTTTTAAAGTCT 45718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTATTTTATACCTTAAAGTTCTTTCACCTATCTTCAGAATTTCAGCTGTTTTTCTCCTA 45658
                                                                                                                                                                                                                      A---TCTCCTCAGGTAAATCTT---
                                                                                                                                                                                                                                                                   ACTATATCTACTGGTAAATCTTTTGCTGTAATCATCTCCTTAGGAGATTTCATAATTAAA 2737
                                                                                                                                                                                                                                                                                                                          TCTCCTATATATATAGGAATTAAATCATCTTTTTCTCTATCAATATTTCTGTTTTTGAAAT 45778
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ilarity 49.3%;
Conservative
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/protesin_id="AA036773.1"
/db_xref="GI:28204335"
/translation="MEYYLMVRIMLYGCNGKMGRIITHCSKDFNDIEIVAGVDKSSTS
NLDFPYFENIHSSSYECDYVLDFSRPSSLKSLISYCTEKKLPLVLCTTGYSKEELNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSIFKGSGVAIVTPFCENGVNFKKLEELIEWHIENSTDAIVICG
TTGBASTMTBAEIKETIKFTVDKVQGRIPVLAGTGSNNTRKALELSKWAKSIGVDGLL
LITPYYNKTTVGKGIVEHFKAINDDVDVPILLYNDPGRTGLMILLAKTLVKICOTCSNVV
AIKBASGDLSQIIBMKALLKDRIDIYSGNDDQIIPILSIGGIGVISVLANIMPKEVHD
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VSGAGMAGYNDLKDGYNGVAÞKKFÞYAIAGNALÞHIDSFLDNGYTKEEMKMVNETRKI
FHNEGLKITATTVRIÞVFNSHSESINVELEKEFNLEDVFELYKNVQGITLEDDVENLV
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ESNLNLLKKELSNHALIK"
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KKIQfcekeftveelkedniknkkidialfsaggtisteyafifvrygatvidnssaw
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/transl_table=11
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/protein_id="AAO36772.1"
/db_xref="GI:28204334"
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/EC_number="4.2.1.52"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="CTC02295"
/EC_number="1.3.1.26"
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/protein_id="AAO36771.1"
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                                                                                                                                                                                                                      CTTTTTTATATATATTGTCTTCTGTAAGCACTATT 45832
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AC134919.3
                                                                                                                                                         AC134919 DNA linear PRI 07-AN Homo sapiens BAC clone RPI3-485B10 from 4, complete sequence
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                       Submitted (07-AUG-2003) Department of Genetics, Washington University, 4444 Forset Park Avenue, St. Louis, Missouri 63108, On Aug 1, 2003 this sequence version replaced g1:25140186.
                                                                                                                                                                                                                                                                  Submitted (01-AUG-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-OCT-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McLellan,M., Haglund,K., Du,H. and Cotton,M. The sequence of Homo sapiens BAC clone RP13-Unpublished (2001)
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Sulston, J. B. and Wilson, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                    Wilson, R.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Waterston, R.H.
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                 Contact: sapiens@watson.wustl.edu
Center project name: H_FH0485B10
                                                             Web site: http://genome.wustl.edu
                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
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arkway, St.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

SOURCE INFORMATION:

The RPCI-13 Human Female BAC Library was constructed using improved cloning techniques developed by Kazutoyo Osoegawa. The library was generated by Bachui Zhao in our laboratory. Construction was funded by a grant from the National Humann Genome Research Institute (NHGRI, NIH) (#1RO1RG01165-03). The library was generated according to the new NHGRI/DOE 'Guidance on Human Subjects in Large-Scale DNA Sequencing'.

Female blood was obtained via a double-blind selection protocol. Female blood DNA was isolated from one randomly chosen donor (out of 10 female donors) and partially digested with a combination of

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/rpt_family="Alu
13134. .13280
/rpt_family="L1"
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10126. .10674
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
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3642. .10125
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Waterston, R
Direct Subm
                                 Direct Submission
Submitted (07-SED-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 122168)
                                                                                                                                            Direct Submission
Submitted (11-AUG-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (14-UUL-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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The sequence of Homo sapiens BAC clone RP11-1388F24
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Sulston, J.E. and Waterston, R.
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COMMENT
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                                                                                                                                                                        Submitted (15-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Sep 7, 2002 this sequence version replaced gi:22203890.
                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu/gsc
Center project name: H_NH1388F24
                            Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                   63108, USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong coworkers at http://www.chori.org pBACe3.6

NEIGHBORING SEQUENCE INFORMATION: This sequence is not the entire insert of the clone. This clone is overlapped by AC015969 and AC130709.

plasmid subclone The sequence from base 48271 to base 48342 was derived from

plasmid The sequence from base 69077 to base 69140 was derived from subclone.

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Best Local Similarity
Matches 1064; Conserv
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                             53330 ATACATTTTATATATATATATATATATATACATTTTATATATATATATATATATATATATACAT 53271
                                                                                                                                                                                                                                                                                                                                                                                    53210 TAATATACATATTÁTÁTÁTATAATÁTÁTATÁ-TÁTAATÁTACÁTACÁTATTATATATATATAT 53152
                                                                                                                                                                                                                                                                                                                         1157 ATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCA 1216
                                                                                                                   1037 GGTCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGT 1096
                                                       1097 GATAATAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATA 1156
                                                                                                                                                                          977 AAATTTCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTATACTCTCT 1036
                                                                                                                                                                                                                                 917 САТАТСТСТААЛАЛАТАСТССАЛТАТТААТТТСТАСТАЛАДСТАГССАДАТТАСАТСАСТС 976
                                                                                                                                                                                                                                                                                             857 ATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACAG 916
                                                                                                                                                                                                                                                                                                                                                    797 GACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATT 856
                                                                                                                                                                                                                                                                                                                                                                                                           737 ATTACACATATAAACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCA 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       677 GCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAAT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 TAAATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 ATACTACTCATCATATTTAGCATAATATCACATCTGACATGATTAACAATAGTAACACAT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.8%; Score 180.2; DB 9; Length 122168; ilarity 45.0%; Pred. No. 1.9e-14; Conservative 0; Mismatches 1273; Indels 30;
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TAAGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAAAATCGTTATGTATATTTA 2296
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                                                                                                                                              TAAACAAATTTCTAATATAACCACCTACTCTAAACATAGGAACCAATAGTATATCATACC 2236
                                                                                                                                                                                                                                                           ATATTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATAA 2056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACAAATTCCTATCTCCTATCTCA 1816
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PUBMED
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                                                                                                                                                                                                                              Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T., Lykidis, A., Bhattacharayya, A., Bartman, A., Gardner, W., Grechkin, G., Zhu, L., Chu, L., Kogan, Y., Chaga, O., Goltsman, E., Bernal, A., Larsen, N., D'Souza, M., Walunas, T., Pusch, G.D., Haselkorn, R., Fonstein, M., Kyrpides, N. and Overbeek, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T., Lykidis, A., Bhattacharya, A., Bartman, A., Gardner, W., Grechkin, G., Zhu, L., Vasaieva, O., Chu, L., Kogan, Y., Chaga, O., Goltsman, E., Bernal, A., Larsen, N., D'Souza, M., Walunas, T., Pusch, G., Bernal, A., Eonstein, M., Kyrpides, N. and Overbeek, R. Haselkorn, R., Fonstein, M., Kyrpides, N. and Overbeek, R. Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586
                                                                                                                        Submitted (13-FEB-2002) Integrated Genomics, Drive, Chicago, IL 60612, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusobacterium nucleatum subsp. nucleatum ATCC 25586
Fusobacterium nucleatum subsp. nucleatum ATCC 25586
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE010598 12277 bp DNA linear BCT 25-MAR-2002 Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 140 of
                                                                                                                                                                                                          Direct Submission
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/mol_type="genomic DNA'
/strain="ATCC 25586"
                                                                         organism="Fusobacterium nucleatum subsp. nucleatum ATCC
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/transi_table=11
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/transl_table=11
                                                                        /gene="FN0897"
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FLAYNNKEFFVIAATLMKGDPDKNKIKHYSLDEVNVQMKNGLLLNGKLILTHSDGKRE
NYRAMKFAFGSLASNNFKKALQKFQ"
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DYLKTVPKKRKIEYHKDDFWSDTPDFEIIFQELNEVKRDDFWEIVPEIKSKFEEEN
DILEDKTYKEBFYIENNERKKELKSKMENYIKEVIFDEKKAMKDEENKNLLI"
COMplement (2417...2800)
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NCKKAKIIVKNKSYIFGL"
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IIKKLEKAGVVKIFRGAKGGYVLTRDPKRLTFRDIIEIIDDDIVLQPCIDSSTICSTR
GADCSIRHALKKIQDDLLDDFDKINFYDLVENNASLQI"
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894. .1316
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MIEWHKKMGHKVFFISGSPSFLVSRMAKKMGVDDFCGSVYEIDEETQTFSGKILKPMW
DSAHKQEAIENFIKKYNIDLSKSYAYGDTNGDFSMLSLVGNPRAINPSKELITRVKND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MDIQFENKYYADDKMGKEYVNKILAKNARGIILLYILIFLFIVK
NGILKGDSGTIFRLIVCTIFLLFLNFLSQKYLFRLLKKTAKSIHNDQSYPTLVQFGNN
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1347. .1883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1347. .1883
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116. .859
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Query Match
Best Local (
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Local Similarity 50.0%;
                                                                                               11496 TAAAAGAAATTTCTTCACTGGGTGTTGCTATGGGT-----GGAGAACAATCTACATTTT 11443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11676
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                                                                                                                                                                                                                                                                                1227
1347 TTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATA 1406
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                                                                                                                                                                                                                                                                                                                                                                                                   AAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTG 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCAGAAGTTTGGCAAAGGAATACCAACTACCTGTGTTGTATCAGCCCATAATAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATTATTGTTAATGTTGCAAAAGGCTTAGAAGAGGATACATTAAAAACTATGACAGATA 11797
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                                                                                                                                                                                                                        GAATAGCTGATGGTCTAAATTATGGAGATAACACAAAAGCTGCTCTTATAACTCGTGGAA 11497
                                                                                                                                                                                                                                                                                                                                           CTGATATGATAGGTGTAGAAATTGGTGGAGCTTTAAAAAATGTTATTGCTCTTGCTGCTG 11557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATTGAGGAAGAGTTAAAGGAAAAAATCCTCAGGTAGCAGTTTTATCAGGTCCTAGCC 11737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTA 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAAAATAAATAGACAAAATAAAACTAAGTTACCTAATATATTACTTCCAGAAGATATAA 11974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATAT 806
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                                                                                                                                                          TGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAA 1346
                                                                                                                                                                                                                                                                                GAATAATCGCTGGAAAAAATTTAAGGTAATAATGCTGTTGCTACTGTTATAACTAAAGGCA 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATAATACCATC 1166
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11202 CAGAAGC--TGTTAATGAACTTATGATAAGAGATAAAAAATTAGAAATACAATCTTGGTA 11145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11442 ATGGACTAACTGGTTTAGGAGATTTAATCGTTACATGTGCAAGTATGCACAGTAGAAATA 11383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1527 ATGTAGAACTACCAATTTGCATATCTATTACAATTTATTACATGAGAATATATCACTAG 1586
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AP004827 BA000033
AP004827.1 GI:21204509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-MAR-2002) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:blo@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baba, T., Takeuchi, F., Kuroda, M., Yuzawa, H., Aoki, K., Oguch
Nagal, Y., Iwama, N., Asano, K., Naimi, T., Kuroda, H., Cui, L.,
Yamamoto, K. and Hiramatsu, K.
Genome and virulence determinants of high virulence
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Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Lancet 359 (9320), 1819-1827 (2002)
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      complement (624. .1283)
                                                                                                                                                                                                                                                                                                                                 complement (278. .619)
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HRLPDYALNOVTNELSYADIKYOLGIJGKNENEKLIKAIDOLEKORILEKLDIAPIDI FGIKASMELHAIDOLEKORILEKLDIAPIDI FGIKASMEJHAIDI KOLHAIGI EGIKASMEJHAIDI KOLHAIGI EGIKASMEJHELNEOLFSTI FTI INDSUYNDDIHRPHNVFTYETKOILKOLHAIDI KLNKTLEI PHOGISHKTYKSLAKOLLLIKOKKYKII EGIKAGHTSFI SI KULSOKSTIR LYVKOYAVKDVLTKOVLEKFKSLIFISGTLKFNHSFEAFKOLFNKDVHFNTFEVNTSL OSAKOTSVFI BSDVASYQYKNIDEYVASIVSYI IEYTTI TSSKCULVLFTSXXMHMVO DMALHELPEFBOYVVLTOQONOYKYLOQFNNEDKAILAGTTFFEGGPDFANGIKCVM DMAKLFFRNENVHLMSESTSTFKEYVLPDAVTRFROGLGRLIRSENDRGIIVSFD
                                                                                                                                                                                                                                                 SLGSGKSLAYLLAALMYNIETGKHVMISTNTKLLQSQLLEKDIPAMNEALNFKINALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="asnS"
/note="ORFID:MW1344"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4ALDEANSLNKLSFKYMDRILLNWKKNNVKTIDDSRKIREKFNKPKMTHTVKTVPKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein, similar to chromosome replication initiation protein dnaD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1273. .1959)
/gene="MW1343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (1273. .1959)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /oodon_start=1
/trans1_table=11
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/protein_id="BAB95207.1"
/db_xref="GI:21204511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="asnS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ORFID:MW1342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ORFID:MW1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="MW1343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .ement(3901, .6594)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _start=1
                                                                                                                                                 SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKVLYNKLQKNMLADIAERFGSELITDQYEYYYQKMLNEHNKSKGE"
complement(10167. .10484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKVREKI PSKLI LLGDGPEL VPMRQLIKELNVEEDVLFLGKQDCVSEFYQLSDLVLLL
SEKESFGLTLLEAMKTGVVPIGSNAGGI KEVI KHGETGFVVDVGDCDSASDYAI RLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (8783. .9925)
/gene="MW1348"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (8783. .9925)
/gene="MW1348"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDLYEDLQRRDFTMMAIAMDTAYKLYDYFDGQQDINNRIIRTVGIAEERFQEDALRMI
RCLRFQSQLSFDIATETEEARRIQMADIKFLSIERIVIELTKLMRGINVEKSFNHLKS
LKAFNYMFYFEHLDMNQINVTEAIDLELLIAIVSVKEPDINYSLKELKSNRQVKDINQ
YIQIMMALFSIITKEQLKMFVYDYDTHLIKNVMVAADVIKANDIQGHEFLIVNLQTID
ETLHRLFMHNRKDMMVNGGVLMAHLNAKSGFWLKDVLRQIEIAIVTGKVSNEETEILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSKYSQDVLQLLYKNKPNYISQQSIAESLNISRTAVKKVIDQLK
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/transl_table=11
                                                                        /note="ORFID:MW1350"
                                                                                                                                                 complement (10820. .11518)
                                                                                                                                                                                   /gene="MW1350"
                                                                                                                                                                                                                  complement (10820. .11518)
                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein"
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/db_xref="GI:21204518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (10167. .10484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AREMSGKDIKIMTTLHGTDITVLGYDHSLQGAIKFGIEKSDIVTSVSKSLAQETHEII
ETNKEIIPIYNFVRENEFPTKHNTALKSQFGIAPDEKVLIHVSNFRQVKRIDTIIETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MKIGITCYPSMGGSGIIATELGIKLAERGHEVHFITSNIPFRIR
KPLPNMIFHQVEVNQYAVFQYPPYDITLSTKIAEVIKEYGLDLLHMHYAVPHAICGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein, similar to lipopolysaccharide biosynthesis-related pr homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trans__table=11
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/TRANIPDBIESIFSHTIPVGKEHGTINVVENDENYEVTTFRAEEDYVDHRREGVTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (7576. .8778)
/gene="MW1347"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (6618. .7589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRLINSNYKNFFEQTLENYRQKKGDIQQFGKLLRQIQKKKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="MW1349"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IWNRTLLFTENDKQFKGQAIDLDYDGYLIVRDEAGESHRLISADIDF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (6618. .7589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="ORFID:MW1349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="MW1349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein, similar to poly(A) polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="truncated hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1/
transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="ORFID:MW1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="ORFID:MW1347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="MW1346"
                                                                                                                                                                                                                                                                                           YGEKKKKDSEEANTIKAELGDNLFVLLCLANSMGIDMTESFNETMEKFNTRDKNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _table=11
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Best Local Similarity
Matches 533; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22554 AGATAAAAGTGTAAGTAÄÄTTÄACGCAAGÄTTTATTTÄTGÄÄTĠÄTTATTTÖCGTGTGTA 22495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22614 GCCAAGTCATGCGGAAGAAGTTGTAGTCAAGCAACCAACTACAGTTGCTGCTTCATCAAA 22555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22734 TAAAAAGACTTTTATACATGTTGCTÄÄAGGTÄTTGÄÄÄATGGGACGTTTÄÄAACGTGTGTC 22675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22905 AAATACATGTCATACAAATAAAAAGTATTTAAAATACGCGAAATTAGATGATGATCAT 22846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22965 TGCAGAAAATGGACATGATGTTTTGATGTGGGGTAAAAATCAAGATGCTGTTGATGAATT 22906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23025 AATGACTĀAĀĀTTACCGTTTTTGGTATGGGĀAGTTTTTGGGĀCĀGCCCTTGCCĀATGTTCT 22966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22788 ACCTACTAAAGCAATGCGAGAAGTTGCTTCTCAAATTAATGATAAGC-----TGACCTC 22735
1519 AAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATAT 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1099 TAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAAATAAT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1039 TCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 AAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTTGGCACAGCAATAGCAATTGCACT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 688 GTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATAT 747
                                                                                                                                                                                                                                                                                                                                                                                                                GACATTTCTAGGTTTAGGTGGTATCGGTGACTTAATCGTTACTTGCACATCAACACATTC 22261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAATAGCAGAAGAAATTTT-----ACAATATAATCCAATTTTTATACTCTCTGG 1038
                                                                                                                                                                                      TCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAA 1518
                                                                                                                                                                                                                                                                     TCGAAATTTCACATTAGGATATAAACTTGGACAAGGTGAATCAATGGATCAAGCATTATC 22201
                                                                                                                                                                                                                                                                                                                                     ACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTGGTTTAGCGGAAATTAGTAGA-----TTAGGTGAAAAGTTAGGTGCCGATCCTAT 22321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAAGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCA 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAAGTGGTATCGTAGCTGGAATTGGCTACGGTGATAATGCAAAAGCTGCATTAATGAC 22375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAATGATTGAAGATTCTATTTCACCTGAATATAATGCAGGTATTGGCGTGTTGTCAGG 22615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAG 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACAGCATATGTGTAA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCTACTTCAGATATGACCAAAGCAATTCAATTTGCAGATATTTACTTAATGG----CTTT 22789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTAT 867
                                                                                                                  TGAAATGAATATGGTCGTTGAAGGTATTTATACAACTAAATCAGTTTATCATTTAGCTAA 22141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTC 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAIQDHQGYWFLRFRAALVPVANLGSSLSYMIIMLGIILTAIGSAFGSTALWIGAGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MSSIFTMIIYFVILMVLPLWAQHKVKSNYEKYSQVRSTSGKTGR/ALALEVG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="conserved hypothetical protein"
/protein_id="BAB95215.1"
/db_xref="GI:21204519"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%;
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Pred. No. 7.1e-14;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim Matches 1029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 3.7%; Score 173.8; DB 2; Length 104992; Local Similarity 46.7%; Pred. No. 1.3e-13; hes 1029; Conservative 0; Mismatches 1122; Indels 52;
                                                                                     72864 АЛАЛАЛАТАВТАСТАЛТТАЛТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛТАЛАТТАЛАТТТТАЛТТАЛАЛ 72923
                                                                                                                                                                                                                                                                                                              72744 ААТАСААТТТАЛАТАТТАЛАТАААТАЛАААТАТТАТАТАТТАТАЛАТДАТДАТАЛАТТАЛ 72803
                                                                                                                                                                                                   22020 GTATTATTACACATATACGGCTAATAAT 21993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22080 CTCAGTAAAAGAATGCGTAAAAAGATTTAATGGAGCGCGATAAAAAATCTGAATAAAATGT 22021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22140 AGAAAAAATGTGGATATGCCAATTACAAATGCATTATATAGAGTATTATTTGAAAATAT 22081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1639 ACACAATGATAAATAAACGGTCAAAAAT 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1579 ATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTCA 1638
525 TCACATCTGACATTAACAATAGTAACACATTTCTTAACACTAGATAATATACAATAA 584
                                                                                                                                                                                                                                                        405 ACTATCTAATTAATAAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAG 464
                                                                                                                                                                                                                                                                                                                                                                   9
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Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 104992)
Hyman, R.W., Oin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hyman,R.W., Fung,B.L., Qin,F., Tamaki,T., Kurdi,O.B., Conway,A.B. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota, Alveolata; Apicomplexa, Haemosporida; Plasmodium.
1 (bases 1 to 104992)
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Plasmodium falciparum chromosome 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum 3D7 chromosome 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC005504.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n Apr 2, 1999 this sequence version replaced gi:4337172. NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                     58843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:5833"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58642: contig of 58642 bp in length 58842: gap of unknown length 91011: contig of 32169 bp in length 91211: gap of unknown length 104992: contig of 13781 bp in length
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2, *** SEQUENCING IN PROGRESS
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	1642 74061	1583 CTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCATTCAT
	1582 74001	1525 TAATGTAGAACTACCAATTTGCATATCTAGTTTACAATTATCATGAGAATATATCA
	1524 73941	1465 CCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAACT
	1464 73881	1405 TATGGCITTTGGACTAGAAATAGGAAAAGGTAGAATATAAATACATTAATAGATCACAA
	1404 73821	1345 AATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAA
	1344 73761	1285 CATGAAGGAAATTAAAACACTATATAGGAAAAAATCATTGAATAGATCTTGATACATT
	1284 73701	1225 IGGAATAATCGCTGGAAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAACTAAAGG
	1224 73641	1169 GATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATG
	1168 73581	1110 TIGGIGAATCATIGAAACAATAAGTA-ATGAIGTTCTAAAAATAATATATCCATCAA
	1109 73521	1051 TAAAGAAATTGCAGAACATCTTCCTTGTAGTAGTAGTACTTGCT-GGTGATAATAAGAAC
	1050 73461	997 AGAAGAAATTITACAATATAATCCAATTITTATACTCTCTGGTCCAAGTITTGC
	996 73401	937 AATATTAATTIGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATAGC
*	936 73341	877 ACAATTACGCACCATATGTACACAAATACAACACAACAGCATATGTGTAAAAATACTCC
	876 73282	817 CAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACA
	816 73223	757 CCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACCAG
	756 73163	697 TGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTA
	696 73103	637 AATCAGTATTTIAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGGACA
	636 73043	585 ATAATATAATITTTGACTGGTTTCTTGATATAATTAGGTAAAAAAATGAA
	72983	72924 TTABATAATAAATATTAATATAAATTAAATTAAATAATAA

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74893 AAATAAATAATTTATAAATAATAAAATATTAATATTGTAGTTA 74935
                                                                                                                                         74833 ATÁTÁAACAATTAÁTTTÁAATTTÁAÁTTTÁAÁÁATTCCATÁAATTÁATÁTTTATÁTÁTTTTT 7489:
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                                                                                                                                                                                                         2406 TCATATCCTTTTTAAAAAGATGACTTCACAATT--CATACATAAATAATTATACATGCAA 2463
                                                                                                                                                                                                                                                                                                                                               2346 TAACAAATTCAAGAATTATATATACTTCACCAACACATAGTTATCAAATTCTATAATACA 2405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2170 ААТАЛАТТАЛАСАЛАТТСТЛАТАТАЛАССАССТЛСТГЛАЛАСАТАССАЛТАСТЛТА 2229
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                                                                                                                                                                                                                                                                                TÄATTAAGAATCATTTTGTGTGTATTATTTTÄÄAÄTÄTTTTTATAAATATATÄÄTTTAA 74832
                                                                                                                                                                                                                                                                                                                                                                                                                  TTRATTTTÄTTTTAÄÄTTÄAÄTTÄTTTATTTCATTÄTAÄATÄÄÄTAAÄTÄTÄTTTATATT 74772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATTTATA----CAATTACAAAATTTCCAACTTCAACAACAAAAACTCAAAGTTCTATTA 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCCAAAAAGGTTAAAATACACATTCCTGCAACAATATGAAGAAGATACAATACACGTCA 2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAACTGTTTTTTTATGCCC-----ATTAGTTCTTAATAAAATTGCTAATT 2109
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RESULT 26 AC004157 LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS ORGANISM AC004157
AC004157.8 GI:9797712
HTG; HTGS_PHASE1.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. AC004157 169546 bp DNA linear HTG 12-AUG-2000 Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.

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REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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                      84568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304, USA
On Aug 12, 2000 this sequence version replaced gi:8810447.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (Dases 1 to 169546)
Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T., Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
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                                                                                                          ATAATATAATAAATTAATTAACAATATTTÄÄÄTÄÄTÄÄTÄÄTÄÄTÄÄTÄÄTÄTATATT 84627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACA 876
                                                                                                                                                   CCGAAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACCAG 816
                                                                                                                                                                                          AAATGAATTATTTAAATAATTAAAACAATAATATATATAAATTAATTATATATTTAGTAA 84747
                                                                                                                                                                                                                                   TGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTA 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACATCTGACATGATTAACAATAGTAACACATTTCTTAACACTAGATAATATACAATAA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACAATTAATTATTATAAATTAAAGAATTATTAATAATAATATATAAATTAATTAAATTA
                                                                                                                                                                                                                                                                                                                       AATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACA 696
                                                                                                                                                                                                                                                                                                                                                                                                         ATAATATATAATTTTTGACTGGTTTCTTGATATAAATTAGGTAAAAAAATGAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Plasmodium falciparum"
|mol_type="genomic_DNA"
|db_xref="raxon:5833"
|chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23466: contig of 23466 bp in length 7 23666: gap of unknown length 7 169546: contig of 145880 bp in length. Location/Qualifiers
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                                                                                                                             85586 TAACATAAAATTATTTATTACTATATATTTAATTAAATAAAAAGTATAAAAATTATCTTTCT 85645
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                                                                                                                                                                     1763 ATAACTTAAAATTTCCTAGCTAATTATATAAACAAATTCCTATCTCCTATCTCAATTAAC 1822
                                                                                                                                                                                                                                                                                                                                         1703 TCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATTTACATAACAAACTTAAGT 1762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1583 CTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTTCAACAC 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1525 TAATGTA--GAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCA 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1285 CATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATT 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1051 TAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCT-GGTGATAATAAAGAAC 1109
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                                           CCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACT 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAA 1404
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        Submitted (13-SEP-2002) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA 3 (bases 1 to 250421)
                                                                                                                                            2 (bases 1 to 250421)
Hyman,R.W., Fung,E., Conway,A., Kurdi,O., Mao,J., Miranda,M., Nakao,B., Rowley,D., Tamaki,T., Wang,F. and Davis,R.W.
                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 250421)
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AE014849 AE014188
AE014849.1 GI:234
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                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
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Submitted (29-JAN-2003) Stanford Genome Technology Center, University, 855 California Avenue, Palo Alto, CA 94304, USA Location/Qualifiers
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VII WRFDNNYKEFÇKI YQMDIKHKSSI KUVAWKENLDNSANI TA KGGDEKI VILWE
DVTNNVKKOGI I KVKYNIKK 150 KGT ILA ILA GGDDKA VILYKENAGGI WEBMCNLI
DVTNNVKKOGI I KVKYNIKK 150 KGT ILA ILA GGDDKA YLYKENAGGI WEBMCNLI
TENNNI 1QDDNSKNYTNAG ÇEKHNENKLANDNNNNNY TGNVAVDSAS YMDN TVASANI
ENNNI 1QDDNSKNYTNAG ÇEKHNENKLANDNNNNNY TGNVAVDSAS YMDN TVASANI
ENNNY PNGSNSL I NENNNLSHQGPY QNKOTHERS ÇGNFAA YNNSTQQQQY SNVOR FDQMNG
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NNKYEPQRYEEYRHNKDERYNNEQDPKTEPQSNINYDKDNNSGRKRNSIDSSRDRKYR
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 997 AGAAGAAAT-----TTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGC 1050
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VPDAGFYENVEILPLKVLFDFIVSSSLPDDIVYFIENDKKKISLNPYEIIYLQIFGLI
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26165 AAATGAATTÁTTTÄÄATAÄTTAAAACAATÁATÄTÄTÄÄÄTÄÄATTÄTÄTÄTTTÄGTAÄ 26405 ĀAAAAĀTAATĀCTĀĀTĀTTAATATĀAĀAĀTĀAAĀTĀATĀĀTĀĀTAĀATTĀATTTTAATTĀĀĀĀ 26346 26525 AATACAATTTAAATATTAAATAAATAAAATATTATAAATTTATAAATAATAATAAATAATTAA 26466 877 АСАЛІТАСССАССАТАТСТАСАСАЛАТАСАЛАСАССАСАЛАСАССАТАТСТСТАЛАЛАЛАТАСТСС 936 817 CAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACA 876 697 TGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAAATATTACACATATAAACACTTA 756 637 AATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACA 696 525 TCACATCTGACATGATTAACAATAGTAACACATTTCTTAACACTAGATAATATACAATAA 584 405 ACTATCTAATTAATAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAG 464 AATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATAGC 996 CCGAAAAATTTTAAAATATTTTACCCACATATCATCTACCAGACAACATATATGCAACCAG 816 /rpt_type=tandem 11322. .11373 /rpt_type=tandem 10548. .10711 Score 173.8; DB 3; Length 250421; Pred, No. 9.4e-14; 0; Mismatches 1122; Indels 52; Gaps 26106

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24916 TTTÄTTTATATTAATTAATTATTTÄÄTTÄTTÄTTÄTTAÄTTAÄTTATTÄÄTTÄÄAAÄTTÄ
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                                                                                                                                                                                                                                                                                                                                                                                                               GTTTGCACACTTTTTCACTACATCATGTATAATAATGAACATAATTTTACATAAAATAACT 1942
                                                                                                                                                                                                                                                                                                                                                                             ATAACTTAAAATTTCCTAGCTAATTATATAACAAATTCCTATCTCCTATCTCAATTAAC 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATTACATAACAAACTTAAGT 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTCAACAC 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAATGTA--GAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCA 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATÁTATATÁTTÁÁTTÁÁTTÁATTATATATATATATTTTAATTTAAATTAAATATATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2464 TGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTA 2506
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                                                                                                                                                                                                                                                                                                                     Submitted (31-OCT-2002) Goettingen Genomics Laboratory, Institute of Microbiology and Genetics, Georg-August University, Grisebachstr. 8, Goettingen 37077, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium tetani E88
Clostridium tetani E88
Bacteria; Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE015939 DNA Clostridium tetani E88, section 4 of 10 AE015939 AE015927 AE015939.1 GI:28203008
                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bruggemann,H., Baumer,S., Fricke,W.F., Wiezer,A., Liesegang,H., Decker,I., Herzberg,C., Martinez-Arias,R., Merkl,R., Henne,A. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1316-1321 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tetanus disease
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                                                                                                                                                                                                                         /organism="Clostridium tetani E88"
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  /product="oxygen-independent coproporphyrinogen III
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20. .1207
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                                                                                                                                                                         _xref="taxon:212717"
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NIISYATVGDNSTAMILEVQEEBIERGFLGHRSFTDSQYIEAIQFPACGMSKIFDKNI
NIEYATVGDNSTAMILEVQEEBIETGTLGHRSFTDSQYEEAIQFBGSFSIEYNELTMDA
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                                                    5833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4390. .5400)
/locus_tag="CTC00859"
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NIAKI INDFKSS I LDVENLMLNNNTNI TGGVR I LTD I VKELKTNI NNLNNVNTDVNE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YINCITENYTI PSNBPCLAI PYFMTFTCLFLNKKI ITVSAI FAPI SEVILLI LKPSLI PLIGENLI I DWTLKUTVU LLNI SGI YLLSVTAANILLEKSSNSEDKLI KNNDKMTNLFNQ I KNI SNTLU I SKDLTTASTSANALQBI SASCYNI NOSBOSVWEDTKKMELI ODLI KNI SNTLU I SKDLTTASTSANALQBI SASCYNI NOSBOSVWEDTKKMKELI ODLI KNI SNTLU I SKDLTTASTSANALQBI SASCYNI NOSBOSVWEDTKKTENSTKELVSI FNKNEBSLNEILSI I YSI KEGTTKTFDSTKFLKNK YSSNOTSDKVVKTGNFSKELVSI FNKNEBSLNEILSI I YSI KEGTTKTFDSTKFLKNK
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/locus_tag="CTC00858"
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KKVKISGIKLSVTVISSLGGKEKMKEHAIETGKAVSLIDPDYLGVLTLLLNEDTKWAE
QVKKGEITLLKPEEVMIETKLMLENWDVTNCIFRSNHASNYVPLKGTLPKDKEKLTRT
                                                                                                             MSLPHNRFTFIADKYGYTGPCSPLLALHDRIQEKPFNESELCIMCSVAAGCIITALLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="chemotaxis sensory transducer protein"
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LKLFNVYDNFELFKLEIYJAVSIIELLILFILHKKIKSNKNFIDDNYNNIGFMFVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIYIQGTRTRIYY"
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RKDYVEPNKKNNNNLLFAFESNPREGQKHIESYNINFANLASDLGYAGGGIAGACTFI
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transl_table=11
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/transl_table=
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/transl_table=
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/protein_id="AAO35453.1"
/db_xref="GI:28203010"
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|518. .1895
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                                             .6921
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                                                                                                      /translation="MMPTINDVAREAGVSISTVSRVLNNNYPVKEETRKRIEEAIEKL
NYKPNNLARSLITKKTSTIGVIVPGITNLEFPFTIVESIEDYSKDGYSIVLCNTRGEA
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YDEKVGTLBAFEYLLELGHKEIAFIRGSKSYSYDIKEKIYTDIIEKNNLKYNEILDVG
KGNSIEVVENTQKKVBEFLLNKNKFTAIFACNDLMALGVVNACNKLNLNVPQDISIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="lac1"
/locus_tag="CTC00863"
9646 ...10650
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KYKGDKFIPVGVDATAPALDSLKAGEMLGTVLNDAKNQGKAIFDIAYSLAKEEDPIK
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              10734. .12287
                                                                             FDNTLISNIIHPKLTTVDLNMKRIGNIAALKLLEIIEDKNKSIKYTMETKLIVRESCY
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/protein_id="AA035460.1"
/db_xref="GI:28203017"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSTSGGIGTVQGIITGVLIFEVLNNGLVILGVSAYWQQVIKGIIIIGAVAFDIRKYIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="galactoside transport system permease protein
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IRTPSHATQIKNLSGGNQQKVIFSRWLLTEPDVLIMDEPTRGIDVGAKYEIYSIISDL
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/protein id="AAO35458.1"
/db_xref="GI:28203015"
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/codon_start=1
/transl_table=11
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005. .8519
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Matches 477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297110 GCAGATATAAACGAAAAAAAAGAAAATATAAAATATCTTCCCAATGTGGTTATTCCATCA 297169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297050 ATTATGTTAGCCAAAAAGGGTTATAACATAAATATATGGGATAGAAAACCCCATGTGATA 297109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296990 AATATGACAATTAAAGGTATAACTTTTATTGGAGGAGGAAGTTTTGGTÄCTGCTTTAGGT 297049
1400 CGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGAT 1459
                                                                                                                                                                                                                                                                                                                                                                                                 1160 TACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATT 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           800 AACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATC 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740 ACACATATAAACACTTACCGAAAAAATTTAAAATATTTACCCACATATCATCTACCAGAC 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             680 ATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 ATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCA 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                       ACCTTTTGGGGGGTAACAGGTATGGGGGGÄTATGATAGTAACCTGTACTAGTATGCATAGT 297754
                                                                                                                                                                                                               AAAGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCAT 1339
                                                                                                                                                                                                                                                              GCTGCTGGTATCTCCGATGGAATAGGATATGGAGATAATACAAAAGCTGCTCTTATGACT 297640
                                                                                                                                                                                                                                                                                                   GCATGTGGAATAATCGCTGGAAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAACT 1279
                                                                                                                                                                                                                                                                                                                                                    ACTAATGATATAATAAGGTGTTGAAATAGGÄGGGGCÄGTGÄÄGAATÄTÄÄTTGCTTTA 297580
                                                                                                                                                                                                                                                                                                                                                                                                                                                AATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATA 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAGTCATGCAGAAGAAGTAGCACAAGATATACCAACTACTGTAGTAGTTACATCAGAA 297460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAGITITGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGAT 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTTATCTCAAATTATAAAAGAAGAATTACCTAAAAATCCTGTGGTAATACTTTCAGGA 297400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTATACTCTCTGGT 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTCTGTACCATCTCATGCTATAAGAGAAATATGCAGAAATATG-----AAAGATTAC 297280
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                                                                                                                      ACATTAATTGGTCCATGATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCA 1399
                                                                                                                                                                     AGAGGAATAAATGAGATAATAAGA-----ATTGGAGAAAAGTTAGGAGGACAAAGGGAA 29769
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KDIAKAKNVPQISYPKCPLCLENVGYKGRLDHPARQNHRVIPVELEEEKWYLQYSPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MIDIKREIERLLIFGKXONLIEEIDKVAARNSLLELFKLDEFYK
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/EC_number="2.7.7.10"
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Pred. No. 9.8
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AP003134/c
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297755 AGAAATAGAAGAGCTGGTCTTTTAATAGGAAAAGGTTTATCTATGGAAGAGGCTATAGAA 297814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I., Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M., Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A., Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C., Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J., Kanahisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K. Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K. Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-JAN-2001) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Jap (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/
Tel:pl-3-3481-1933, Fax:81-3-3481-8424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 301550)
Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Hosoyama A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
Direct Submission
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Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome, section 6
AP003134 BA000018
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21311952
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                                                                                                                                                                                                                                         / LTAIAI ALLON="MSS.IFMMIIYFVILMVLJPLMAQHKVKSNYEKYSQVRSTSGRTGR
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                             complement (1001. .1588)
/gene="SA1294"
                                                                                                                                     complement (1001.
                                                                                                                                                                      AELVRIILIARSSD"
                                                                                                                                                                                                    SLAVLFSIVTLPVEFDASSRAMKQITALNIVNEKEYKHARKVLSAAAMTYVAATAVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Staphylococcus aureus subsp. aureus N315"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (249. .947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SA1293"
note="ORFID:SA1294"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="ORFID:SA1293"
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YQMEVASAQVKSAILFASLFSNDTTVIKELDVSRNHTETMFRHFNIFIEAERLSITTT
PDAIJHIKPADFHVPGDISSAAFFIVAALITPESDVTTHNVOINFTREGIIDIVEKMG
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COMDLOMENT (1578. . 2153)
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LDFLKTLPFEQILSGYAEVYKHALLNGESTTQEIEQHFKDREILGSLNGMDKYIAKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNIQLFNQTTGASFTASIRIQYTPMLQFITIEGELVFKAIDELFVIALLCTQAVGTST
IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3418. .4716)
/gene="aroA"
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LEIEHGDANEGVLLLKQALEVDNAYQEPLLILSDLYRNEEDYEAIIELLTYVDBEDLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGLMPQGLEVFRVLYHKYPDESELLIYFIEGLMSENQTDEALEYLSYVEPSPEKLMLE
ADLYQQINMMEVAIDKLQEALELEPNDPIIHFALAEMLYYDGQYLRATSEYETVLETG
EYQVNGVNLFSRMADCSLQSGNYSDAIRLYDEINEDEMTSEDYLKKAISYDKNDITQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (4726. .5790)
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/gene="SA1296"
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                                                                                                                                                                                                                                                                                                                                                                                                                                complement (4726. .5790)
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                                                                                                           Local
   628 AAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACT 687
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Similarity
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grvveiggikdlvggwynhedlrnvlerssaretaarvavcalckvilogliig
grvveiggikdlvgfybeffyhhedlrnvlersydbiaproyserfykaarysgsiddei
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Complement (5816. .6982)
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/protein_id="BAB42563.1"
/db_xref="GI:13701269"
                                                                                                                                                                                                                                                                                                                                                                       complement (8318. .9277)
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (7368. .7568)
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/trans table=11
/product="chorismate synthase"
/product="delanate"
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/transl_table
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="ORFID:SA1301"
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                     Score 172.8; DB 1
Pred. No. 1.2e-13;
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Indels
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RESULT 30
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                                                                                        11447 GTATTATTACACATATACGGCTAATAAT 11420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATAT 747
                                                                                                                                            ACACAATGATAAATAAACGGTCAAAAAT 1666
                                                                                                                                                                                                                                                          ATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTTCA 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACATTTCTAGGTTTAGGTGGTATCGGTGACTTAATCGTTACTTGCATATCAACATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTC 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCAAGTGGTATCGTAGCTGGAATTGGCTACGGTGATAATGCAAAAGCTGCGTTAATGAC 11802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAAT 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAAGTCATGCGGAAGAAGTTGTAGTCAAGCAACCAACTACAGTTGCTGCATCATCAAA 11982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAATAGCAGAAGAAATTTT-----ACAATATAATCCAATTTTTATACTCTCTGG 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAAAGACTTTTATÁCATGTTGCTÁÄÄÄGGTÄTTGÄÄAAATGGGACGTTTAAACGTGTGTC 12102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCTACTAAAAGCAATGCGAGAAGTTGCTACTCAAATTAATGATAAGC-----TGACCTC 12162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTAT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMATACATGTCATACAMATAAAAAGTATTTMAAAATACGCGAAATTAGATGTTAACATCAT 12273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATA 807
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                                                                                                                                                                                                CTCAGTAAAAGAATGCGTAAAAGATTTAATGGAGCGCGATAAAAAATCTGAATAAAATGT 11448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAÄATTTCACATTAGGÄTATAAACTTGGACAÄGGTGAATCAÄTGGATCAAGCÄTTATC 11628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTGGTTTAGCGGAAATTAGTAGA-----TTAGGTGAAAAGTTAGGTGCCGATCCTAT 11748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCATGTGGAATAATCGCTGGAAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAAC 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACGAATGATGACTTGATTGGTGTTGAACTTGGTGGTGCATTGAAAAATATCATCGCAGT 11862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAAT 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAAACCACTGATATCATTAGCAAA 1518
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Clostridium tetani E88, section 3 of 10 of the complete genome.
AE015938 AE015927
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Clostridium tetani E88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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/393. .8022
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Matches 517;
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                                                                                                                                                                                                                                                                 127005 TTTAGAATTGAACAGATAAAATGTAGTGTTTTCCTTACATTTGACTTTCTAATGTTGTT 126946
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                                                                                                       TGCTGAACGTTCCATTCCAACAAATTCAGCAGTTCGTGATACATTACCTCCAAAACGA-- 2572
                                                       TGTTTAGCTATCTTTTCATACAAAGAGGTTCTACTTATATTCAGCTTCTTAGCTGCTAAT 126826
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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dakrigkntpcakigycvdckssericnyftvikgqfksrikviivnkhlgy"
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/locus_tag="CTC00588"
/complement (8089...9645)
/locus_tag="CTC00588"
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/locus_tag="CTC00591"
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EQEIKKANYNTCIBEVMSEFPSFTQYEVRAALAKCGLTTKHIESKVLVLSGGEQAKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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/protein_id="AA035204.1"
/db_xref="GI:28202780"
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;omplement(11177
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Pred. No. 1.2e-13;
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Kanamori, M.,

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                                      REFERENCE
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                                                                                                                                                                                                                                                                                                                         RESULT 31
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             AUTHORS
                                                                                        ORGANISM
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Staphylococcus aureus subsp. aureus
                                                          Staphylococcus aureus subsp. aureus Mu50
Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                         sequence, section 5/9.
AP003362 BA000017
           Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
                                                                                                                                                                      AP003362.2 GI:14247083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTATGTATTAGCCTAGCAACTACTTCCTTTCCAACACCTGGCGAACCAGTAATGAGT 3352
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology, 1-1- Ten-noodai, Tsukuba, Ibaraki 305-8877, Japan (E-mail:tohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 29, 2001 th
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Location/Qualifiers
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4939. .5436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="SAV1318"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="SAV1317"
                                                                                                                                                                                 note="similar to two-component sensor histidine kinase"
                                                                                                                                                                                                                      gene="SAV1321"
                                                                                                                                                                                                                                                                                                            'gene="SAV1321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="similar to ABC transporter integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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Best Local Similarity
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199193 TÁÁAÁAGACTTTTATÁCATGTTGCTÁAAGGTÁTTGAAÁATGGGACGTTTAAACGTGTGTC 199134
                                                                                                                                                                                                              199247 ACCTACTAAAGCAATGCGAGAAGTTGCTACTCAAATTAATGATAAGC-----TGACCTC 199194
                                                                                                                                                                                                                                                                                                                                                 199304 CGCTACTTCAGATATGACCAAAGCAATTCAATTTGCAGATATTTACTTAATGG----CTTT 199248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199364 AAATACATGTCATACAAATAAAAAAGTATTTAAAAATACGCGAAATTAGATGTTAACATCAT 199305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199424 TGCÁGAÁAÁTGGACATGATGTTTTGATGTGGGGTAAAAÁTCÁAGATGCTGTTGATGAATT 199365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199484 AATGACTAAAATTACCGTTTTTGGTATGGGAAGTTTTTGGGACAGCCCTTGCCAATGTTCT 199425
                                                                                                                                       928 AAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAG 987
                                                                                                                                                                                                                                                                              868 TCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACAGCATATGTGTAA 927
988 TGAAATAGCAGAAGAAATTTT------ACAATATAATCCAATTTTTATACTCTCTGG 1038
                                                                                                                                                                                                                                                                                                                                                                                                                        808 TGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTAT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            748 AAACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              688 GTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATAT 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 AAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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/trans| table=11
/product="thermonuclease"
/protein_id="BAB57466.1"
/db_xref="GI:14247095"
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/gene="SAV1323"
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/protein id="BAB57484.1"
/db xref="GI:14247093"
/db xref="GI:14247093"
/translation="MTSLIIAEDQNMLRQAMVQLIKLHGDFBILADTDNGLDAMKLIE
/translation="MTSLIIAEDRIKKHLNIKVIIVTTFKRPGYFEKAVVNDVDAYV
LKERSIEELVETINKVNNGEKEYSATLMTSEFVDKNPLTFKRQIVLRBIGNGLSKEI
SEKLFLTDGTVRNYTSVIIDKLFADNRFDAMKKANEKGWI"
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/gene="SAV1323"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein id="BAB57485.1"
/db_xref="G1:14247094"
/translation="MWISNENTVTLIAVIIAIIIGIFLQIFFKLPLIVTAVLSILLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="SAV1324"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 172.8; DB 1;
Pred. No. 1.1e-13;
0; Mismatches 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 24; Gaps
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RESULT 32
CJ11168X4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                  JOURNAL MEDLINE
                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                        DAMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1039 TCCAAGITTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGA 1098
                                                                                                                                 Parkhill,J., Wren,B.W., Mungall,K., Ketley,J.M., Churcher,C., Basham,D., Chillingworth,T., Davies,R.M., Feltwell,T., Holroyd,S., Jagels,K., Karlyshev,A., Moule,S., Pallen,M.J., Pann,C.W., Quail,M., Rajandream,M.A., Rutherford,K.M., VanVliet,A., Whitehead,S. and Barrell,B.G.
The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences
                                                                                                                                                                                                                                                                                                                                                                                   Campylobacter jejuni subsp. jejuni NCTC 11168
Campylobacter jejuni subsp. jejuni NCTC 11168
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
  2 (bases 1 to 282183)
Parkhill, J.
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AL139077.2 GI:6968444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        segment 4/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campylobacter jejuni subsp.
                                                                                                          Nature 403 (6770), 665-668 (2000)
                                                                                                                                                                                                                                                                                                                                                           Campylobacteraceae; Campylobacter
                                                        .0688204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAGTAAAAGAATGCGTAAAAGATTTAATGGAGCGCGATAAAAAAATCTGAATAAAAATGT 198480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTCA 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATAT 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAAATGAATATGGTTGTTGAAGGTATTTATACAACTAAATCAGTTTATCATTTAGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGAAATTTCACATTAGGATATAAACTTGGACAAGGTGAATCAATGGATCAAGCATTATC 198660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACATTTCTAGGTTAGGTGGTATCGGTGACTTAATCGTTACTTGCATATCAACACATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTC 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCAAGTGGTATCGTAGCTGGAATTGGCTACGGTGATAATGCAAAAGCTGCGTTAATGAC 198834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACGAATGATGACTTGATTGGTGTTGAACTTGGTGCTTGAAAAATATCATCGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGATGTTCTAAAAATAAT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAAGTCATGCGGAAGAAGTTGTAGTCAAGCAACCAACTACAGTTGCTGCATCATCAAA 199014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAAAAATGTGGATATGCCAATTACAAATGCATTATATAGAGTATTATTTGAAAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCA 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGTGGTTTAGCGGAAATTAGTAGA-----TTAGGTGAAAAGTTAGGTGCCGATCCTAT 198780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCATGTGGAATAATCGCTGGAAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAAC 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282183
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jejuni NCTC 11168 complete
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JOURNAL
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Submitted (09-PEB-2000) Submitted on behalf of the Campylobacter sequencing team, Sauger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_jejuni/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Cj1009c"
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/noce="Cj1009c"
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/trans1_table=11
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/note="Cj1010, tgt, probable queuine
/note="Cj1010, tgt, probable queuine
tRNA-ribosyltransferase, len: 373 aa; similar to many e.g
TGT_ECOLI queuine tRNA-ribosyltransferase (EC 2.4.2.29)
(375 aa), fasta scores; opt: 1016 z-score: 1190.9 E(): 0,
41.3% identity in 373 aa overlap. 56.7% identity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="tgt"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GOA:Q9PNT1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HP0281"
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                                                                                                                                                                                            note="Cj1011, probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="tgt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Cj1009c, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:192222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Campylobacter
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tRNA
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SBS
                                                                                                 VKAAS LHAQBALEGSNRPODES FWLWFKSAWLEVGRTIMLISTEGEPQNWKNSLLLHFK
DFALSNENKALELIGSNRPODES FWLWFKSAWLEVGRTIMLISTEGEPQNWKNSLLLHFK
DFALSNENKALELIGSNALKLELS YKNESKEFVI FEVYKKPIALOKFFI SWALSY
EQLPFDI YLRDFYLDR YPGSMS PAS YASEI TVKNNNENPDYRI FWNYLDYDGYRFYQ
SSYDODEKGTYLSVNKDFGRI PTYI IGYFLLCLGMFMNELNPHGRFRTLARLINKDTLK
HTSVI I FILLES FGGEKIFAODLNSTLEVVNTWHAKALATLIV OKSADGRAVVPDTLK
REILEKIHQSDS YKGQNSNAVMLSMLVDDWGQLEFFI LMPQNQA VRDA IANI LEI IS
RKYIAYKD FFDENNRYKLOKYVEBANRKSPNAGOVFDKEI IKLDERAMVVNIN VFSGEL
FKEI PVQNNPNNWLAPFSAVTTLKGDEGHI VLALI (DYFSAVENAFKDGNVIRADEG
LKFI KEYQEKI GYKVMPSKTKVEMEI FSUKALE IFVKLAPVYLI AGFILLILUFSKMVV
PNLKI SFI IKVVYVLNULAFV IHTVGLGLRAYLSGHAWSNGYESMYLAHLSLYGI
FFSRKSFTALSCHAWAHLSBMNPQITNLVPVLNSYMLSHVSVUTTASYGF
LGLCALLGI FTLFLMCFLKKDGKYNLNI IRNI TEATR I NEMAMI FGLCLLTUGNFLGA
IWANESWGRYWSKUSKETWALVSI LYVXALIHLRNI PSYCNQFVEALMSMRAYWVIIN
TYFGVNYFLTGLHSYAAGEAQI PNYVYWGFALMVVLAFFARRKRNFVGKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spanning domains; aa 90-780 is non-membrane, and aa 780-1081 contains ten possible membrane spanning domains. Some similarity in C-teminal membrane spanning domains. Some similarity in C-teminal membrane domain to eukaryotic proteins e.g. CCSA_CHLRE cytochrome C biogenesis protein CCSA_(353 aa), fasta scores; opt: 459 z-score; 515.4 E(): 2.1e-21, 36.0% identity in 267 aa overlap, and to prokaryotic equivalents e.g. CCMF_ECOLI cytochrome C-type biogenesis protein CCMF_(647 aa); BLAST9 scores; E = 0.20, 24% identity in 293 aa overlap, 39.0% identity to HP0378.
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IDTLYTLTNAIKNEKNKKSIYLLSILSSIFLPLNLIVGFFGNNTNNLFFKDSPYGTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (3961. .7206)
/gene="Cj1013c"
/note="Cj1013c, probable membrane protein, len: 1081 aa,
/note="Cj1013c, probable membrane protein, len: 1081 aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVIFCAALALLLFLGVIAYLITSDGKKTIKKQKT8QKQHVAEKT
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                                                                         complement (7224. .7919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILPIREHTQNSLIESSKTSLRISAIKDGERYSAVNDRYIGNLPFANSFKLKLNLGDDQ
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NDNVKAPFVKIDENLTLSSSENLHFLSMLDGQNLDLKIGEKANAKERRLYEINDISFV
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/gene="Cj1012c"
complement (7224. .7919)
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/transl_table=
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                                /gene="livF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             len: 1081 aa;
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Matches

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Query Match
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                                                                                                                                                                                                15585
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3139 ATGATTTGCTTGCTCTATAATTCCAATATGAGGAGGTACTCTATGAGACAATATATTATT 3198
                                                                                                                          2899 TTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATATAAATCCTCACA 2958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PS00211 ABC transporters family signature"
complement(7797, .7820)
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transporters, score 147.40, E-value 2.5e-40"
complement (7482. .7526)
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NALINSVKRTGEVNFLGYDTKRHLTHTLVQKGIALVÞEGRRVEINLSVEENLKIGAFN
NAENYEHLÆGMYKLFPRLASKKHALAGTLGGGEAQMLAISRALMSEPKLLMLDEPSL
GLAPKIVGEVFDIIVRLKEEGITILLVEQNAYSALKISDYAYVLENGRIVMENBAKNL
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                      1076 ÁCGTTACCTGACCÁGTGGTÁTTCCATCÁTGCAATGTÁÁÁCTTTGCTGGTGGAGCÁCTTTG 1017
                                                                                                                                                             2708 ATCATCTCCTTAGGAGATTTCATAATTAAAATCCATTCTATAACATTACGTAATTGTCTT 2767
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                                                                                                                                                                                                                                                                                                                                                                                              for diagnostics and therapeutics
Patent: US 6605709-A 2580 12-AUG-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breton, G.L.
Nucleic acid and amino acid sequences relating to Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
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                                                                 AAGTTACCTGGCCATTCATATGACTGCATTGCTATTAAAAGCTTCATCACTTAATACATGA 2827
                                                                                                               ATAATCTCTTGGCTAGCGGTCATAACCGTTAACCAACGACATACGTTTTCTAATTGTCTG 1077
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                               3665 ATATCAG 3671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3485 TOTATAGCTCTCTTTACAACTAACTTAATCTTCCTTCTGTAAAAAGGCTTTTCTATATAA 3544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3368 GTAGCTGCTTTATTAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTATT 3427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3308 CTAGCAACTACTTCCTTTCCAACACCTGGCGAACCAGTAATGAGTATACGACTCGATGTA 3367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3188 AATATATTATTACTTTCCTCACTACCAAATATATTAACCAAGTAATTATTAGCTGGTAGC 3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3008 ATAATTCTCACATCTATACTAACAGGAATCTTACTATTTTCCCTATATATTTTTCCCTCC 3067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2948 АААТССТСАСААААССТАССАGСТТТАСТТСАСТТТСААТАТСТТТGGAAGAAGACACA 3007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1016 GTTTCAÁCÁCCAAGCTCTCGAGCGGTTTTTTGGÁGAAAATAACGCGCCTAAGCTTGGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2828 GTACACAAACCTATTTTTTACAGATGCTATTCATAAAATACCTACACAATTCCGGTATA
                                                                                                                                                                                                                                                                                                                                    182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 TGTGCAACTAATTCTTTACCAGTACCCGACTCGCCATTGATAAGCACACTAATTGATGAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 GTAATAGCACGATGAATGAGTGCAAGTGTATCATCAATATCAAAAGGCTTGGGGAGATAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 CGAGAAAGGCGGCCAATAATGCGATAAACCTCTTGCATCGCAGGGGGCTTCGCCAATCATG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          596 ATA----TTGAGTGCAATAAAAGGGGCTTGTGCTCTCGGACTATGGCGATGAAGAGCA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   716 AÁGAGGGAACCGCCATTTGCTTGTTCAÁAACGGCCTTGGCGTACTTGAGATGCACCAGTA 657
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                                                                                                                                                                                                                                                                                                                                                                                                                             242 ATAATAACCGGCAACGTAGGGTGTTGCTCTTTAACGCTTTTTAATAGAGATAAACCATCA
                 Clostridium acetobutylicum
Clostridium acetobutylicum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                               complete genome.
AE007680 AE001437
AE007680.1 GI:15024666
                                                                                                                                                                                   \Delta E007680 10861 bp DNA linear BCT 27-JI Clostridium acetobutylicum ATCC824 section 168 of 356 of the
Clostridium.
                                                                                                                                                                                                                                                                                                                                 ATATCAG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATAAGCACCCATATGCAGAGACTTTACAGCAGTGGCAATATTACCATGCCCACTAATC 3604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGAGACAGATTGAAGGTTAGTTTCTGTTGTATTAGGTTGTTTTTTGCTCTCGATAGTGC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGTACAATATTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATAT 2947
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REFERENCE

(bases 1 to 10861)

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JOURNAL
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JOURNAL
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J. Bacteriol. 183 (16), 4823-4838 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 10861)
Childress,D., Zeng,Q. and Smith,D.R.
Direct Submission.
Submitted (24-JUL-2001) GTC Sequencing Center Production,
Finishing, and Bioinformatics teams, Genome Therapeutics Corp., 100
Beaver Street, Waltham, MA 02453-8443, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Clostridium acetobutylicum"
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Query Match
Best Local Simi
Matches 498;
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                               8495 GGGCTT---
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                                                                                                                                                                                                                                               CATAATACCCTGCTGCGTTAAAGCAGTAGATGATATTGAGAAGG---CAGCTAAGGAAAG 8434
                                                                                                                                                                                                                                                                                                   TCATCTACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAA 846
                                                                                                                                                                                                                                                                                                                                                       TAAAGAAATTCTTGAAGATATAAATACATTAAGAACTAATACAAGATATCTTCCAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACAGCACTTGCAATAATGCTTGCTAAAAAAGGTCATAATGTTGTGATTTGGGATAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACAGCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCTTGATATAAATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGG 666
                                                                                                                                                                                           TACATGTATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACA 906
                                                                                                                                                                                                                                                                                                                                                                                                              TCATAGAAATATTACACATATAAACACTTACCGAAAAAATTTAAAAATATTTACCCACATA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S JAKGMEEETKKRLSBVVKEBLYKNPVVVLSGPSHAEBVANDI TTVVVTSTDNKKAE
BVQDVPMTNS FRVYTNSD I VGVEIGGAVKNI I ALASGIGDGI GYBDNTKAALMTRGMS
EIMRI GVKLGGKPETFFGLTGMGDLI VTCTSMISRNRKAGI LI GRGMSCKEACDKI GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAKPLVTIVGRPNVGKSTLFNKLAGKRVSIVEDTPGVTRDRIYA
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VNKFKSEGEDEEEEEYIKIAFVGKPNVGKSSLTNRILGEERVIVSDIPGTTRDAIDSF
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6902. .8218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNNKFAGNLMERMKKLSNAGITMNCQVVLCPGINSGEEFSKTVNDLYKLYPSVKNIAG
VPVGITSYRSGLFNMVPYDSQSALKEIENIKF1QEKFIKBIGSPVRLSDEFYVLSGI
PIPKALEFYGEFEQFEDGIGMIRTFRNNIMMSLDLKDGGIHKSFTMVTGVLAYEBIENA
AKMLMEKSRGLKINVIKVINEFFGEKITVAGLLTGRDILNYLKRNEVGDYIILPSNML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CAC1713"
9300. .10778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LETDFGKLVLIDTAGLRRKSRIKEEIERYSAVRTMAAIERCDVCTLILDATEPISEQD
ERIIGYAHENNKAILVIVNKWDLIEKDDKTMENFKKNLEMKFSFMAYAPFLFISAKTG
QRVHKVLSEIKKCYDNYSKRIATGVLNDVISNAVLMKEPPVVAFKRLKIFYVTQTDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSDEDVFLDDVKVLDIEKELNKKVLVCNYSGEDLVDIINKNGREE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRKTLYFKDDDSRLSFLQGNFVTLTNMSDDDIDRIIKYRISPINISVQTTNPELRKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVEGVKACHTFYELKESLGVSMPITTSLYKVLFENGDPKKEVYELMARDKKNEYYF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPTF1FFVNNPELLHFSYRRYLENKLRQSFDFEGTG1KM1FKERKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="CAC1712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAK79677.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="Predicted GTPase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="CAC1712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.5%;
                            TTTAAGAGAAGACCAAATAATTATAAGTATTGCAAAAGGCATGGAAGA 8548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
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MEDLINE
                                                                                                                                    TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             967 TACATCACTCAAATTTCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTT
                                                                                         Direct Submission
Direct Submission
Submitted (29-MAY-2003) Microbiology, University of Texas
Submitted (29-MAY-2003) Microbiology, University of Texas
                                                                                                                                                                                                                                                                                                1 (bases 1 to 3900)
Yang,X.F., Alani,S.M. and Norgard,M.V.
The response regulator Rrp2 is essential for the expression major membrane lipoproteins in Borrelia burgdorferi proc. Natl. Acad. Sci. U.S.A. 100 (19), 11001-11006 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme disease spirochete)
Borrelia burgdorferi
Bacteeria, Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
Borrelia burgdorferi group.
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Borrelia burgdorferi NlpD (nlpD)
                                                                                USA
                                                                                                                                                                                      2 (bases 1 to 3900)
Yang, X.F., Norgard, M.V. and Alani, S.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACATTAATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAAACCACTGAT 1506
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                                                 Location/Qualifiers
/organism="Borrelia burgdorferi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:33520757
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Best Local S
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Local Similarity 49.5%;
                                      3021 CTATACTAACAGGAATCTTACTATTTTCCCTATATATTTTTCCCTCCTGTAATAATCTGA 3080
                                                                                                                                                                                2961 ACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGAAGACACAATAATTCTCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2661 TAATAGGCGAATTAGATACTATATCTACTGGTAAATCTTTTGCTGTAATCATCTCCTTAG
                                                                                                                                                                                                                                                                                                                                                                                                   TTTCCTTTGCGACGTCTTTTATTAGTATGTTTGTTAAATAAGATATATCATCTTTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTTTTACAGATGCTATTCATAAAATACCTACACAATTCCGGTATATCTGTACAATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTTTGATAATATTAATGCGCTTTCAAGCACATTTTTAATTCTCTAATATTTCCTGGCC
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                                                                                                               CTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATATAAATCCTCACAAA 2960
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/translation="MSKILVADDEKNIREGIATYLEDEGYFTTASTCHERGKSLLMGKIFELTEK
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/protein id="AAQ21217.1"
/protein id="AAQ21217.1"
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to ORF BB0761 in Borrelia burgdorferi strain B31 genome"
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|strain="297"
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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 133877)
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Maylor, J., Myyen, C., Nicol, R.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Direct Submission
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Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., Chang, C., 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                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu

Center_project Information
Center_project name: 124769
Center_clone_name: 2146_H_24

Center_clone_name: 2146_H_24

Center_clone_name: 2146_H_24

Center_clone_name: 2146_H_24

Center_clone_name: 2146_H_24

Center_clone_name: 2146_H_24

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 132654 bases at least Q40

Consensus quality: 132665 bases at least Q20

Consensus quality: 132665 bases at least Q20
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Insert size: 133000; agarose-fp
Insert size: 13577; sum-of-contigs
Quality coverage: 17.1 in Q20 bases; agarose-fp
Quality coverage: 17.0 in Q20 bases; sum-of-contigs
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3.6%;
Best Local Similarity 45.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   682 TGCACTGTCAGCACATGGTATA---TCAGTTAACTTATGGGGACGTGATCATAGAAATAT 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 TACTCATCATATTTAGCATAATATCACATCTGACATGATTAACAATAGTAACACATTTCT 561
                                                                                                                                                                                                                                                                    622 TAGGTAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAAT 681
                                                                                                                                                                                                                                                                                                                                                         562 TAACACTAGATAATATACAATAAATAATATATATTTTTGACTGGTTTCTTGATATAAAT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 GCAAGAACTACAAATATAATGAGACACTTAACTTATTAATATTTCAAATTTATTATAC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 ATCAATCAAAACAAAATAATAGTACTATCTAATTAATAAAAAATCCTCAATAGTCTTTA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              799 CAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTAT 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the finished sequence as soon as it is available and the accession number will be preserved.

1 716: contig of 716 bp in length
717 816: gap of 100 bp
817 1487: contig of 671 bp in length
1488 1587: gap of 100 bp
1588 1993: contig of 406 bp in length
1994 2093: gap of 100 bp
2094 133877: contig of 131784 bp in length.
                                                                                      ТАСАСАТАТАААСАСТТАССБАААААТТТААААТТТТАСССАСАТАТСАТСТАССАБА 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 168.8; DB 2;
Pred. No. 5e-13;
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	1878 AATATGTTIGCACACTTTTTCACTACATCAIGTATATAATGAACATAATTTTTACATAAAA 1937
	1818 TTAACCAATTGTTATCAGATTATAAATAAGTCAAATTAAACTTTTACTTTATTATAAAAT 1877
	1758 TAAGTATAACTTAAAATTICCTAGCTAATTATATAAACAAATTCCTATCTCCATATCTCAA 1817
	1698 AGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATACATAACAAACT 1757
	1639 ACACAATGATAAATAAACGGTCAAAAATATAGAATACAACGTTCACCACATAT-ATAAAA 1697
R (1579 ATCACTAGATAAAGCCATAICAAACATATTATCTTAGTCTATCATCCTTTGATAATITCA 1638
2 K S A S	1519 AAAACTTAATGTAGAACTACCAATTTGCATATCTATTACAATTTACTAGAGAGATAT 1578
	1459 TCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAA 1518
	1399 ACGCAATATGGCTTTTGGACTAGAAATAGGAAAAAGGTAGAAATATAAATACATTAATAGA 1458
2 2 5	1339 TACATTAATIGGTCCATCATGTCTIGGAGATCTAATATTAACATGTACAACAGAACATTC 1398
9 2 8	1279 TAPANGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCA 1338
2 2 8	1219 TGCATGTGGAATAATCGCTGGAAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAAC 1278
2	1159 ATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAAT 1218
5 5 8	1099 TAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAAT 1158
, g ,	1039 TCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTAATTAAGTACTTGCTGGTGA 1098
, g ,	979 ATTICCCAGIGAAATAGCAGAAGTATTTACAATATAATCCAATITTTATACTCCICGG 1038
	919 TATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAA 978
	859 CTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACAGCA 918
ð Ē	94483 TATTATATAATATATATATTATATATTATATATATATA

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KEYWORDS
SOURCE
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    JOURNAL MEDLINE
                                          TITLE
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Hall,N., Pain,A., Berriman,M., Churcher,C., Harris,B., Harris,D., Mungall,K., Bowman,S., Atkin,R., Baker,S., Barron,A., Brooks,K., Buckee,C.O., Burrows,C., Cherevach,I., Chillingworth,C., Chillingworth,T., Christodoulou,Z., Clark,L., Clark,R., Corton,C., Cronin,A., Davies,R., Davis,P., Dear,P., Dearden,F., Doggett,J., Feltwell,T., Goble,A., Goodhead,I., Gwilliam,R., Hamlin,N., Hance,Z., Harper,D., Hauser,H., Hornsby,T., Holroyd,S., Harrocks,P., Humphray,S., Jagels,K., James,K.D., Johnson,D., Korhornou,A., Knightes,A., Konfortov,B., Kyes,S., Larke,N., Lawson,D., Lennard,N., Line,A., Maddison,M., Mclean,J., Mooney,P., Moule,S., Murphy,L., Ollver,K., Ormond,D., Price,C., Quail,M.A., Rabbinowitsch,E., Rajandream,M.A., Ruthers,S., Rutherford,K.M., Sanders,M., Simmonds,M., Seeger,K., Sharp,S., Smith,R., Squares,R., Squares,S., Stevens,K., Taylor,R., Unwin,L., Whitehead,S., Woodward,J., Sulston,J.E., Craig,A., Newbold,C. and Barrell,B.G. Woodward,J., Sulston,J.E., Craig,A., Newbold,C. and Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
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Plasmodium falciparum MAL4P3.
AL035476 AL844503
AL035476.7 GI:23498195
                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAAAAAGATGACTTCACAATTCATACATAAATAATTATACATGCAATGTTTATTCAGAA 2476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAATTATATATACTTCACCAACACATAGTTATCAAATTCTATAATACATCATATCCTTT 2416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTATATTTAT
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On Oct 3, 2002 this sequence version replaced gi:5763808.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12368867
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TSATLSGGBSAFTENPCELIKDKODELLGDSGBEHFCGNGSASEKRESEVSGGECDDK
KIEGNGRNNNGGACAPYRRLFLCNKNMEKOGRTSTTKHDLLLDVCMAANYEAQSLIRYH
DQYDATYFGSDFSNCTMLARSFADIGDIIRGKDLYLGKKKKTETERDQLESKLKKI
FGDIYNELIMGRNGVKDHYQDDNGGNYFQLREDWWTANRAITWKAITCKADTGNAYFR
PTCSNRQGFSQAHHYCRCNGDKPDDKFNTDFYTFYTDYVPGYLRWFEBWAEDFCRKKK
IYUGIVKTYCREKKKSGGNEFXVGRNGYNCDTKTRAIGSSSNYDGYESKFYNILKDDY
WINNOKEQFDXQKKKYTDEINEASRSSRROKRGARSTGSSSNYDGYESKFYNILKDDY
GTVDDFLKLLNKEKSGAVADNDGGTINFTEKNDDKNNNNKDGTFYRSEYCOVCPDC
GVKYNGSLYDFWQCYQFDQLEXDEKEEGVDDRNTDNYTGGGLCILGXXNGGENGKK
QGNSDSLYDFWQCYQFDQLEXDEKEEGVDRNTNNNKGGGLCILGXXNGGENGKK
QGNSDSLYDFWQCYQFDQLEXDEKECCLQNGTKTRCRNNEKCNKEGECFGRWVEKK
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QKTYNDFNFWYAHNLSSIHWKKKLEKCLQNGTKTRCRNNEKCNKEGECFGRWVEKK
QKTYNDFNFWYAHNLSSIHWKKKLEKCLQNGTKTRCRNNEKCNKEGECFGRWVEKK
QKTYNDFNFWYAHNLSSIHWKKKLEKCLQNGTKTRCRNNEKCNKEGECFGRWVEKK
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                                                                                                                             PDDEEDLLLEENENQVAQPNICPNQVEDKKIEEEVEKCETAQTTAEETAAAGGERQTP
PAPAPAAPPSPPRPLPKPKPPKPDLPPALKNAMLSSTIMMSVGIGFAAFTYFFLKKKT
KASVGNLFQILQIPKGDYDIPTLKSSNRYIPYASDRYKGKTYIYMGDSSGDEKYAFM
                                                                                                                                                                                                                                                           KTTYPSKYCKACPYGVKY1GNY1PNEBKDYKSKKGRVKKBNDT1PKNIEVJUJGRK
GEEKDKDKHLHDACKTTGLFBYARYEØMNCQKKKGIDQCKITKFANDIIPFDKDIVFU
PFQRWLRYFYQDYNKLKDKINPCTKKETEKEKSKSYKCTQGCNDKCECVKEWLSKKKQ
EWTQIKTLYKQYSKLSDQEIAFRVKSYEVDQGLFDNDYKKAQEVVEKPCDKEKLMGCT
GDNLKEGEDPGKCHMGDFITNLISKLQKKIDDCNKNQAQNSVETQPSDENTAQCQDTH
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CRNIDKAGHHYCSGDGYDCTRDVIERNDKFVDLNCLGCYKQCRKYKKWIDIKFVEYHN
CEKKYKDEYGKLTKDKSSDDKKLEGYKCAENFLKELKHCKPSEDNNDQDNKINFDKPE
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QRRDTDSSGDTTGGKDGATGGLCIPPRRRRLYVGGLSQMASQRTQGETSSQSGENLLE
AFIQSAAIETFFLMHKYKAENTKTQGVGAGGADFLPATSSVATALAPGAVPSRPSLQL
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HLSEMLQETSGDGLTCGASDNEXETLMDKLI EHEEGI AKECLRKQNECEKKAKPEGRS
DSHDDPQPPDDADNEDDLDDEDDEDEEEEVQVEDNTQEEGEQFVVPQQEEGSSSFTPA
PITDDEWNQLKHDFISNMLQNTQNTEPNILHDNVDNNTHPTMSRHNMDQKPFIMSIHD
RNLFSGEEYNYDMFNSGNNPINISDSTNSMDSLTSNNHSPYNDKNDLYSGIDLINDAL
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PLITLLRPGVLGNGLQS PQSRLRTLDGHFAGGESEDKTPQQWLQQGHIPDFLRLMFYT
LADYRDI.GJGGDRDI.VGDTI.VSNTEGSSSSKIKISEKIKELINHDNKQEPARKSSVEK
LADYRDI.GJGGDRDI.VGDTI.VSNTEGSSSIT.EDKDVRDKLI.DKDTGKPQKNGDNDYT
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/gene="PFD0630c"
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/gene="PFD0630c"
                                                                                        SDTTDVTSSESEYEELDVND!YVPGSPKYKTL!EVVLEP$GNNTPTSD!P$DNTPTPÇ
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/db_xref="GI:23498196"
/db_xref="GOA:QBI1V7"
/db_xref="SPTREMBL:QBI1V7"
/db_xref="SPTREMBL:QBI1V7"
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|mol_type="genomic DNA"
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/chromosome="4"
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SGNHIDIYDEMLKRKENELFGTQHHPKNITSNRVVTQTSSDDPIHNQLNLFHTWLDRH

CDS

/note="Similar to Plasmodium falciparum rifin pfc1115w, mallp7.54 SWALL:097311 (EMBL.AL034559) (371 aa) fasta scores: E(): 4.8e-58, 49.73% id in 382 aa, and to Plasmodium falciparum rifin pfb0035C SWALL:096113

complement (join (28486. .29547, 29708. .29776))

/note="synonym: RIF"

gene="PFD0640c"

gene

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misc_feature
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ABETTAAAGGERQTEPAAPAEAPEPEPEPLFKEKFEKPDLPALKVAMLSSTIMMSVGI
GFAAFTYFFLKKKTKASVGULPGILOJENGDVDIPTLKSSNRVIEPASBTRYGKTYIY
MEGDSGDEKYAFMSDTTDVTSSESEYEELDVNDIYVPGSPKYKTLIEVVLEPSGNNT
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NDLYSGIDLINDALSGNHIDIYDEMLKRKENELFGTQHHPKNITSNRVTTQTSSDDFI
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EFTNMDTSPDKSTMDTIIDDLEKYNEPYYYDFYEYDIYYDVNDDDKTSMDNNNNLVNK
NNFVDSNSSTYNHHNPADINKTFVDINNHNQHPIEKPTKIQIEMNSNNREVDEQQYPI
                                                        NSNNREVDEQQYPIADIWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDIDFDKDIVFNEFFQRWLRYFVQDYNKLKDKINPCTKKETEKEKEKSYKCTQGCND
KCECVKEWLSKKKQEWTQIKTLYKQYSKISDQEIAFRVKSYFVDQGLFDNDYKKAQEV
VEKPCDKEKLWGCTGDNLKEGEDPGKCHWGDFITNLISKLQKKIDDCNKNQAQNSVET
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complement(join(17269. .18690,19611. .25169))
                                                                                                                       DKTSMDNNNNLVNKNNPVDSNSSTYNHHNPADINKTFVDINNHNQHPIEKPTKIQIEM
                                                                                                                                                                                                                                         HNQLNLFHTWLDRHRDMCEKLKNDNERLAKLKEEWENETHSGDINSGIPSGNHVLNTD
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LESKLKEIFGDIYNELTNGRNGVKDHYQDTTDYFQLREDWWTANRHTVWKAITCGTHE
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lltsatlsggesaftenpcelikekrekllgargernpcgngsasekrfsevsggecd
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/product="erythrocyte membrane protein 1 (PfEMP1)"
/protein id="CAD49167.1"
/db xref="GI: 23498197"
/db xref="GOA:Q8I1V6"
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(join(28486. .29547,29708. ..29776))
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Best Local Similarity
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                                                               67574 TAATTAAAATAAAAATAATAATCATATAAATATAAATTAATTAAAAATAA-AATAATAAT
                                                                                                                                                        67334 ATĀAĀTAĀĀTĀTĀTĀTATĀTĀTĀTĀTĀTĀĀĀARATĀAĢĀCATTAAATTAATTTATTATAAAAT 67393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67274 TAATAAATTGTGTGATAAGAATAATTTACAATTTTCTTTTATTAATGATAATTATATAAA 67333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 ACCTCTTCTCTTGTTCCATCCATATTTTCCAATTATTTACAATATCATAGAGTTCTTTAT 364
                                                                                                                                                                                                                                                                                                                                                                        600 TGACTGGTTTCTTGATATAAATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGAT 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 CAATAGTAACACATTTCTTAACACTAGATAATATACAA----TAAATAATATATAATTTT 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 ATTTCAAATTTATTACTACTCATCATATTTAGCATAATATCACATCTGACATGATTAA 543
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840 ACAACAATACATGTATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACAC 899
                                                                                                                                                                                                  720 GACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAAAATTTAAAATATTTAC 779
                                                                                                                                                                                                                                                                                      660 CATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTG 839
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OKIILKDKIEKELTEKLGALQTEIRSDAIPTCTCQKSVGYKVEKTCLKCGGILGVGVA
PSLGLLGEIGGLVINNWKNT PFYEAFVAFAQKEGIAAGKARAKIDTVISGIISNF
EVHTINGSTLAMAITLETKADDTILTKALHFEYGSMCVNTPTDDKLICAYGRAFALDV
GKSASPEAVIRSSVKTLLKNADNVASQAAQTTANETTSGMIKAELSKIASAGANTYSA
ITYSVTAILVIVLMVIIYLILRXRKKKKKKKKKLQYIKLLKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between residues 24 and 25 Similar to Plasmodium falciparum Rifin, mallp4.02 rifin SwALL-(99NPB5 (RWML-AL031747) (331 aa) fasta scores: E(): 9e-53, 50.43% id in 349 aa, and to Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Signal peptide predicted for mallp4.07 by SignalP
2.0 HMM (Signal peptide probabilty 0.895, signal anchor
probability 0.008) with cleavage site probability 0.389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.52% id in 386 aa"
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/product="RIFIN"
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join(34475. .34549,34788. .35753)
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/translation="MKVHYISILLFSHPLNILLTSSQVYNQKNPYLTPHKTNPKSVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAD49168.1"
/db_xref="GI:23498198"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene≈"PFD0645w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 168.8; DB 3;
Pred. No. 3.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 1622; Indels 56; Gaps
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                                                                                                                                                                                                                                                                                                             68686 AATTATATATTTAAATTATAATATATAATAATTAATTCGTTAATTTATTATTATTATT 68745
                                                                                             68112 TTAATATAAAATATAAAATAAAATAAATTATAAATGTTAATTAATTAAATAAATAAATATAT 68171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1920 АСАТААТТТТАСАТААААТААСТААТАААААБААССААТАСАТАТАТТАААТТАСТАААА 1979
                                                                                                                                                                                                                           1800 TCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATTATAAATTAAAGTCAAATTAAACT 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1560 ATTTATTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTA 1619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1380 CATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAA 1439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ТСАТССТТТGАТААТТТСААСАСААТGАТAААТAAACGGTCAAAAATATAGAATACAACG 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATAAATTAAATATTATATATATATGCATTAAAATTAAATAAT---
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68926 AT-TAATTAAATTTAATTTATATATAATAGTTTATAATAAATTAATTTAATTTAATTTATTTG 68984
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                                                                                                                                              69705 AAATTAAATTATTATAAATAAATAAATGAAAATTTATATAATTAAGAGTAAAATTAA 69764
                                                                                                                                                                                                                                                        2745 CTATAACATTACGTAATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATTGCTATTA 2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2685 CTACTGGTAAATCTTTTGCTGTAATCATCTCCTTAGGAGATTTCATAATTAAAATCCATT 2744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2220 СААТАСТАТАТСАТАССТАДСТААСАТАТСССТАСАССАТСТАТСАЛАТАЛАТАЛАДАЛАА 2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2160 ATACACGTCAAATAAATTAAACAAATTTCTAATATAACCACCTACTCTAAACATAGGAAC 2219
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                                                                                  2979 CACTTTCAATATCTTTGGAAGAAGACACAATAATTCTCACATCTATACTAACAGGAATCT 3038
                                                                                                                                                                                                2919 TAATTGGAAGGACATTTAATCTATAATATAAATCCTCACAAAACCTACCAGCTTTTACTT 2978
                                                                                                                                                                                                                                                                                                           2859 TCATAAAATACCTACACAATTCCGGTATATCTGTACAATATTCTACTAAAGACGGTACTC 2918
                                                                                                                                                                                                                                                                                                                                                                                                                     2805 AAGCTTCATCACTTAATACATGAGTACACAAACCTATTTTTTTAC-----AGATGCTAT 2858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3219 TATTAACCAAGTAATT 3234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3039 TACTATTTTCCCTATATATTTTTCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTAT 3098
     1046 TITGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAA 1105
                                                                                           358 ATTGAÁGÁTTCTATTTCACCTGAÁTÁTAÁTGCAGGTÁTTGGCGTGTTGTCAGGGCCAAGT 417
                                                                                                                                              995 GCAGAAGAAATTIT------ACAATATAATCCAATTTTTATACTCTCTGGTCCAAGT 1045
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                                                                                                                                                                                                   298 ACTTTTATÁCATGTTGCTÁÁÁÁGGTÁTTGÁÁÁATGGGACGTTTÁÁÁCGTGTGTCAGÁÁÁTG 357
                                                                                                                                                                                                                                                           935 CCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAATA 994
                                                                                                                                                                                                                                                                                                              244 AAAGCAATGCGAGAAGTTGCTTCTCAAATTAATGATAAGC-----TGACCTCTAAAAAG 297
                                                                                                                                                                                                                                                                                                                                                                   875 CAACAATTACGCACCATATGTACACAAAAACACACAAACAGCATATGTGTAAAAATACT 934
                                                                                                                                                                                                                                                                                                                                                                                                                           187 TCAGATATGACCAAAGCAATTCAATTTGCAGATATTTACTTAATGG---CTTTACCTACT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           815 AGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACA 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 TGTCATACAAATAAAAGTATTTAAAATACGCGAAATTAGATGTTAACATCATCGCTACT 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   695 CATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AATGGACATGATGTTTGATGTGGGGTAAAAATCAAGATGCTGTTGATGAATTAAATACA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masignani, V.C., Mora, M.C. and Scarselli, M.C. Staphylococcus aureus proteins and nucleic acids Patent: MO 02094868-A 5629 28-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5629 from Patent W002094868.
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                                                                                            REFERENCE
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                                         AUTHORS
                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                         TITLE
                                                                                                                                 PUBMED
                                                                                                                                                                                                                                                                                                                     Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Cronin, A., Davies, R., Davis, P., Dearden, F., Doggett, J., Feltweil, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holfroyd, S., Horrocks, P., Humphray, S., Jagels, K., James, K.D., Johnson, D., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Line, A., Maddison, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rutter, S., Rutherford, K.M., Sanders, M., Seger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Squares, R., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Parrell, B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 CATGCGGAAGAAGTTGTAGTCAAGCAACCAACTACAGTTGCTGCTTCATCAAAAGATAAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      658 TTAGCGGAAATTAGTAGA-----TTAGGTGAAAAGTTAGGTGCCGATCCTATGACATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 AAAGAATGCGTAAAAGATTTAAT 974
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Murphy,L., Pain,A., Berriman,M., Bowman,S., Churcher,C., Harris,B. Harris,D., Lawson,D., Quail,M., Rajandream,M., Hall,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
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                                                                                                                                                                                                                Sequence of Plasmodium falciparum chromosomes 1, Nature 419 (6906), 527-531 (2002)
                                                                                                                                                                                                                                                                                                       Barrell,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           šukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barrell, B.

Direct Submission
Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium,
Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein but pfam match and other evidences suggest that it is a putative decayribonuclease; earlier start site possible to make a 412 am protein pfam match to entry pro1026 TatD DNase, TatD related DNase, score 117.30, E-value 2.9e.31
Similar to Plasmodium falciparum conserved hypothetical protein, upf0006 family mallp3.01 SWALL:Q9U0N6
(EMBL:AL031746) (412 am) fasta scores: E(): 3.7e-150, 100% id in 412 am, and to Saccharomyces cerevisiae putative decoxyribonuclease yb1055c yb1055c or yb10511 SWALL:PBF5 YEAST (SWALL:P34220) (418 am) fasta scores: E(): 2.5e-19, 30.47% id in 397 am"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein c119.18 spbc119.18 SWALL:Q96VGi (EMBL:AL022117) (69 aa) fasta scores: E(): 1.3e-06, 39.68% id in 63 aa, and to Homo sapiens protein 15e1.1 15e1.1 SWALL:15E1_HUMAI (SWALL:043715) (76 aa) fasta scores: E(): 0.00046, 38% id in 50 aa, and to Mus musculus protein 15e1.1 15e1.1 SWALL:Q9D8Z2 (EMBL:AK007514) (76 aa) fasta scores: E():
                                                                                                                                                                                                                                                         /protein_id="CAD49076.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein, conserved"
(protein id="CAD49075.1"
/protein id="CAD49075.1"
/db_xref="Gari-34477099"
/db_xref="SpTREMBL:081227"
/translation="MENRSKTISONTIKAHVEANDECKEKKEKYLKCFNNWYKNNFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWALL: Q9D8Z2
0.00054, 38%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: MAL1P3.01"
complement(join(1392. .1461,1752. .2598,2748. .2848,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (join (201. .257, 455. .586, 748. .804))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Originally annotated as Plasmodium falciparum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="PFA0580c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Similar to Schizosaccharomyces pombe hypothetical
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                                                       /note="synonym: PFA0585w"
3005, .5496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="TatD-like deoxyribonuclease, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                          /gene="MAL1P3.02"
                                                                                                                                                                                                                                  IKCDDNTIFKERNEPYNIADIAEITYKVREBAVPFDLFCKK'
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gene SGD

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/note="contains possible signal sequence. Signal peptide predicted Signalp 2.0 HMM (Signal peptide probabilty 0.640, signal anchor probabilty 0.357) with cleavage site probability 0.504 between residues 27 and 28. ScanRegExp hit to PS00867, Carbamoyl-phosphate synthase subdomain signature 2"
                                                                                                                                                                                                                                                                                                                                                       NIRSMILFGNEYNPLIYKYTILQSELLNDLSTIEHGDMKYINDDHNLSKGÓKVRICLA
RALYEHYIHMHKLCTDYEKKLIQPNEILDKDLINKWISSLKVKKSKLVNYNIFPNEN
YLQKCLMDDNNFYLYLLDDIFTSLDPSISKKIFSNLFOKLÖNISFKDNGSFIISMKS
TLDNFLIEDILDNUQYEVNIFELQDKTLKYRGNISEYNEKNNLNITKESHWGYSNLNI
IDYTRIKLFDEVELNHVKHSNKMIYKEAYFVKONTESVSFEIDSINKBYIKXMKKKNY
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KKEHMMKONKDNNNNNNSNKDDHININMDNHRNDSHFOSSINKINNSSINSTENSTEDSSF
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FKGSISLETYLMYFQQVGFVLLTSVVIIMLISIFTDEIKFVFLTMMSIISKNNKEHSD
TILDKOVRYLEYFVILETISLTTSGIGFSMIIYGNITBAIKFVFLTMASIISTANALTH
                                                                                                                                                                         YNNNLGNIINFEIIDISAFDYGFLKRIYKAFFIFFRCILSSLLIIYMIRDCIFIFPFV
IILIYEFVFKKESRGCKEAQRLYLSCHTPLCNIYSNALSGKNILNIYKKNTYHLDVYE
HYINNFRISYFFKMLNIWASLIYKIFILLLTIYIIMPHLYASGIIKLYKEKNYVRI
LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEBFAKISNKEMASKNIKENI
NVITTQYYKEKNENISDKISAIVEYKNVSLSSIINSSQDDESKKKYGIKFENVYVSYK
KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSIIGLINISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI
YLKORLNKKEBIKFTSIMPLIVYKLILSNVANFENLVNNVNEGIVNIKRLINYINDH
LYYNDIKMYFMYRITXIBEDYNIVVDKTFLQNENITSHDDGTSHNLKHLKNVIKNKLINDH
MFKVFFFFYHKMNYHKNIINKQILSGLLKOVDDNTNKKICFQEHKGNSTYVNSSHIHB
KKEBYENIHNSSNSTMSNEFKEKKKNNBYIIKLENCSFGLSYDNKCDNDHILKNINFN
LKRNSLAIIIGNVGSGKSAFFHSILGDENMTHGNLYIENFFKKMPILYVPQNSWLFMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NHLQNPDAFYNTYRKFSSQTEIDEISRDFLSIGKNASSSSGIKNNNKNIDNNKFVEN
DYIINFIKSTKKMEKDSLNENRSLENVNIYNIMFSDVPSVTFFVTSCINLFNVFVKIF
MSFYVFHIKIGSNSVGIAIWLSIALYSAMILFEFLPSLFKSKYLIYRDKRIDNMHFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDIQELPNICKNFDVPYYASKLEENLKDIEVEDSEFYSEKNSSNEHVLHHCNSNDASE
KXVYNVYYHNILMSILKTFKFRIILIISFYILETLIVTLGGKFIDYYMRILEGQKIPV
YISFLKDFXVFSGLVVVMIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Putative ABC transporter
Pfam match to entry PP00005 ABC tran, ABC transporter,
score 45.00, E-value 1 7e-09; HMMSmart hit to SM00382,
ATPases associated with a variety of cellular activities;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signature 2"
                                                                                    KITVEGRDIRTYNRKGEDSIIGILAQSSFVFYNWNIRTFIDPYNNFTDDEIVHALKLN
GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLINDCIRYLSLVRLYLN
RHKYKIILIDEIPIFNLNNSVHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transporter abc1 abc1 or spac9e9.12C SWALL:ABC1_SCHE
(SWALL:Q92337) (1427 aa) fasta scores: E(): 4.2e-08.
21.46% id in 1146 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similar to Schizosaccharomyces pombe ATP-binding cassette transporter abc1 abc1 or spac9e9.12C SWALL:ABC1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Putative centromere"
14884. .20352
/gene="MAL1P3.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="hypochatical protein"
/protein_id="CAB63557.1"
/nb_xref="GI:6594245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="ABC transporter, putative"
/protein_id="CAB63558.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ScanRegExp hit to PS00211, ABC transporters family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="mkllunrfyvlcpiiilffflusvvlgnunnnuinfhetenaak
amrkllsgeinsikldngdelkiklndekhkdstkwdksysfisnleeekysqtdlfr
                                                    LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:Q9UON4"
/translation="MTTYKENVGISNKGNKKKKSCQNISFLNFLSEDWIRPLINDLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB63558
/db_xref="GI:6594246"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db xref="SPTREMBL:Q9U0N5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xref="GOA:Q9U0N4"
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Best Local
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                                                                                           8181 AAATAAATAAAATAAAATAAATATTAAAAAAATATAAATTAATAATAATTAATTAATTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8011 TATAGTACACATTTATATTAATAAATATA-----ATTAAAGAATATTTTATCTTT 8060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7771 TĊTĀAĀTĀTTTĀTTTGAĀATTACGAATTATAĀTTTTCTATGAAAGGTACTTTTATAAĀTA 7830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7717 TATATGTATTATATTTCTTTATTGAATTGCT-----CTCATTAATAGTACTTAGATGTT 7770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              508 TCATATTTAGCATAATATCACATCTGACATGATTAACAATAGTAACACATTTCTTAACAC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 ACTACAAATATAATGAGACACTTAACTTATTAATATTTCAAATTTATTATACTACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 CAAAACAAAATAATAGTACTATCTAATTAATAAAAAAATCCTCAATAGTCTTTAGCAAGA 447
867 TTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAACAGCATATGTGTA 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 AAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCAC 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 TAGATAAT-ATACAATAAATAATATATATTTTTTGACTGGTTTCTTGATATAAATTAGGT 626
                                                                                                                                                      927 AAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCA 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTA 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ТАЛАСАСТТАССGАЛАЛАЛТТТАЛАЛТТТАСССАСАТАТСАТСТАССАGACAACATAT 806
                                                                                                                                                                                                                                                                                                                                      rgrcagcacarggrafarcagrraacrrarggggacgrgarcaragaaararracacara 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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complement(join(31966. .32476,32675. .32775))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="ITS2 A-type"
/note="ribosomal operon internal transcribed spacer 2
expressed in asexual stage parasites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26560. .27435
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/product="5.8s ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="ribosomal operon internal transcribed spacer l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="18s rRNA exppressed in asexual stage parasites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="28s ribosomal RNA (A-type)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="5.8S ribosomal exppressed in asexual stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="ITS1 A-type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="mall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lt to vivax A-type 5.8S ribosomal percent id: 88.00 none"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 1541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8srNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 168.4; DB 3
Pred. No. 7.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 67970;
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7950

/product="18s ribosomal RNA A-type"

9135 1887 9194 1947 9254 2007 9314 2067 9371	1587 8895 1647 1707 9015 1767 9075	1287 8595 1347 1347 8655 1407 8715 1467 8775 88775	8301 1047 8361 1107 8416 1167 8476 1227
İDADAİTİAATATİATTAATÄÄİTTAATÄÄÄTTATAAİTATTATAİÄÄTÄÄÄÄÄÄÄÄ		TGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAA 1346	ATTADATADAATATTAAAAATATAAATAATAATAAATAA
QY QY QY Db Db RES		0	S B S B S B S B S

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3021 CTATACTAACAGGAATCTTACTATTTTCCCTATATATTTTTCCCTCCTGTAATAATCTGA 3080
                                                                                                                                                                                                                                                                                2961 ACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGAGACACAATAATTCTCACAT 3020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2841 TTTTTTACAGATGCTATTCATAAAATACCTACACAATTCCGGTATATCTGTACAATATT 2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2781 ATTCATATGACTGCATTGCTATTAAAGCTTCATCACTTAATACATGAGTACACAAACCTA 2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9911 TTATATTAAAACTAAATTAATTAATATAAATTAATATATATATATTAATATTTAATTAAT
                                                          3081 GTAATCTTAATTGCGTATCGTAAATCTGTTACTTCAT 3122
                                                                                                                                                                                                                                                                                                                                                                                                    2901 CTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATATAAATCCTCACAAA 2960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2725 ----TITCATAATTAAAATCCATTCTATAACATTACGTAATTGTCTTAAGTTACCTGGCC 2780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2485 CAATCCAAGAATTTTCAATTTACGGTGTAATGCTGAACGTTCCATTCCAACAAATTCAGC 2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9731 TAATATATTAAATTAACTTTAAAATAATATTTATTATTAATGTATTATATCATTATTAT 9790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2427 GACTTCA--CAATTCATACATAAATAATTATACATGCAATGTTTATTCAGAAACATTACA 2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2367 ATACTTCACCAACACATAGTTATCAAATTCTATAATACATCATATCCTTTTTAAAAAAGAT 2426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2307 AAATTTCCAACTTCAACAACAAAACTCAAAGTTCTATTATAACAAATTCAAGAATTATAT 2366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2127 ТАСАСАТТССТВСЬАСАТАТВАВСЬАВАТАСЬАТАСАСВТСЬВАТЬВАТТЬВАСЬВАТТ 2186
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1 (bases 12511 to 12882)
Clary, D.O., Goddard, J.M., Martin, S.C., Fauron, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster complete mitochondrial genome.
U37541
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Nucleic Acids Res. 11 (8), 2411-2425 (1983)
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Analysis of nucleotide substitutions of mitochondrial DNAs in
Drosophila melanogaster and its sibling species
Mol. Biol. Evol. 4 (6), 638-650 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic code
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                                                                                                                                                                                                                                                                                    8 (bases 14917 to 19517)
Lewis, D.L., Farr, C.L., Farquhar, A.L. and Kaguni, L.S.
Sequence, organization, and evolution of the A+T region of
Drosophila melanogaster mitochondrial DNA
Mol. Biol. Evol. 11 (3), 523-538 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        evolutionary considerations
Genetics 118 (4), 649-663 (388212147)
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                9 (bases 1 to 408; 13319 to 19517)
Lewis, D.L., Farr, C.L. and Kaguni, L.S.
Drosophila melanogaster mitochondrial DNA: completion of the
nucleotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)
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Ballard,J.W., Olsen,G.J., Faith,D.P., Odgers,W.A., Rowell,D.M.
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Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9558-9562 (1990)
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Lewis, D.L., Farr, C.L. and Kaguni, L.S.
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LKSGAAPEHEWEPNMEGLIMMMALIKATULERSSILLLAFEYSTLSFVLTFMENIF
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/product="cytochrome c oxidase subunit II"
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complement(1322. .1
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organelle="mitochondrion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (1403.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="tRNA-Cys"
complement(1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="cytochrome c o:
/protein_id="AAC47812.2"
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|oin(1470..1472,1474..3009)
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                                                                                                                                                                                                                                                                       transl_except=(pos:3767,aa:TERM)
transl_table=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSTIGSTISLLGILFFFFIIWESLVSQRQVIYPIQLNSSIEWYQNTPPAEHSYSELF
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East Lansing, MI 48824-1319, USA
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                                                                                                                                                                                                155 ATTGATATCTAGAAGCAAACCATTTTCTCAAATCTCCAATTTTAACATGCACAAGATTAT 214
                                                                                                                                                             215 TTAATGTAACAGAACACCCTGTACTCTTATGCAAGAACTCTATAAACTTATCAAGGTCTC 274
               AATTATTTACAATATCATAGAGTTCTTAT-TCGACATACATATTAAAATCAATCAAAAC 393
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=5
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LSLALPLWLCFMLYGWINHTQHMFAHLVPQGTPAILMPFMVCIETISNIIRPGTLAVR
LTANMIAGHLLLTLLGNTGSSMSYMLMTFLLMAQIALLVLESAVAMIQSYVFAVLSTL
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/transl_table=5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MPQMAPISWLLLFIIFSITFILFCSINYYSYMFNSPKSNELKNI
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                                                                                                                                                                                                                                                                                                                                                                                                     /product="tRNA-Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="tRNA-Gly"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         product="tRNA-Ala"
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                                                                                                                                                                                                                                                                       Score 167; DB 3; Length 19517;
Pred. No. 1.7e-12;
0; Mismatches 2240; Indels 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1114 ТGAATCATTGATAGAAACAATAAGTAAT-GATGTTCTAAAAATAATATACCATCAAGATA 1172
                                                                                                                                                                                   1290 АТGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAATTG 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            814 CAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTAC 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694 ACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACAC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 AAAATAATAGTACTATCTAATTAATAAAAAAATCCTCAATAGTCTTTAGCAAGAACTACA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        634 GAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGC 693
                                                                                                                                               GATATATAATAATATATAAATATTTATATATATAAATATCTATTAATTTATAATTAG 17724
                                                                                                                                                                                                                      ACAACAATTACGCACCATATGTACACAAATACAACACAACAGCATATGTGTAAAAATAC 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAAC 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTATTTTTAAAAAACATGATTTTAT-----TATATAAATATTTTTTATAAAAATAAT 18486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAGCATAATATCACATCTGACATGATTAACAATAGTAACACATTTCTTAACACTAGATA 573
                                     CTTTTGGACTAGAAATA-----GGAAAAGGTAGAAATATAAATACATTAATAGATCAC 1462
                                                                          GTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGG 1409
                                                                                                                                                                                                                                                                                               AGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGG 1113
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14916 TÍAAAGTTTTATTTTGGCTTAÁAÁATTTGTTÁTTÁATTTGATTTATATGTAAATTTTTGÍ 14857
                                                                                                                                                                   15334 AAAAAAAATTTTTTTTAGTCATTTAAAAGAAATTAATCTATAATTTTTTAAAATTTTTT 15275
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                                                                                                                                                                                                                                                                                     4012 TAAACATATTATAAAAATTAGTTACTATT--ATTACTAATTTATCAAGCATAGGTTTCCT 4069
                                                                                                                                                                                                                                                                                                                                                                                  3833 ACTTCAGAAATATACAATCTTTCCTTGGACATTTCAAAATCCTGTGCCATAATTACCTAC 3892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3653 СТГААТССАТСААТАТСАGATССТСТТААССАТАТАТССААТААТАСААСАТСАGGCTCT 3712
                                  4190 GTCTATAGTTTTCCATACTAAAAACTCACTTGAAGCTTTATAGATATTCAATAAT 4244
                                                                                                                                                                                                          4070 ATATATCCAAAAAGAAAATAAAAACACTTAATAAAAACTTATCATCAACTTTGTAAAC 4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3893 AATACTAATGAAATACTGCAAACACA-ATGTACTCCTTTAAAGTACACCTCATAATACTA 3951
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Search completed: April 5, 2004, 18:26:33 Job time : 18045 secs

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Run on:
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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8558.496 Million cell updates/sec
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Sequence 3206, Ap
Sequence 350, App
Sequence 513, App
Sequence 1399, Ap
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Sequence 11, Appl
Sequence 60, Appl
Sequence 32, Appl
Sequence 20, Appl
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                                                                                                                                                                                                                                                                                                             Sequence 23, Appl
Sequence 73, Appl
Sequence 14, Appl
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Sequence 6, Appli
Sequence 333, App
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Sequence 300, App
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
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; Patent No. 6605709
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; LENGTH: 1425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
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PRIOR FILING DATE: 199-04-09
NUMBER OF SEQ ID NOS: 8344
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3068 TGTAATAATCTGAGTAATCTTAATTGCGTATCGTTAATCGGTAAATCTGTTACTTCATCATA 3127
                                                                                                                                                                                                                                                                                                                                                                                           2888 TCTGTACAATATTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATAT 2947
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                                                                                                                                                ATAATTCTCACATCTATACTAACAGGAATCTTACTATTTTCCCTATATATTTTTCCCTCC 3067
                                                                                                                                                                                                                 AGATETTEAEGAAAATCAEETTECATTAEGEGTTTTTETAAGTETTGATGAGTEGEGGEA 837
                                                                                                                                                                                                                                                                    AAATCCTCACAAAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGAAGACACA 3007
                                                                                                                                                                                                                                                                                                                                 TCTTCTGTTCTATCACGCAGTGGGGGCAATTGAATACGTATTACATTGAGTCGATGGTAG 897
                                                                                             ÁTAATACGCÁCATCGÁCTTTCACÁGGGGCATAACCGCCAACACGATAAAATTGTCCTTCA 777
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; Sequence 3206, Application US/09328352
; Patent No. 6562958
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 3206

LENGTH: 1557
                                                                                                                                                                                                                                     Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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1148 AGCTGACGAACATTACCAGGCCATGGTAATTGTTGCATATAGTCCGTTGTTTCAGTGCGT 1089
                                                      2759 AATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATTGCTATTAAAGCTTCATCACTT 2818
                                                                                                          1208 TCTTCTGGATAAACCTCACGACCAGTAATCATGACGGTTAACCAACGGCAGGTATTTTCA 1149
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                                                                                                                                                        TTTGCTGTAATCATCTCCTTAGGAGATTTCATAATTAAAATCCATTCTATAACATTACGT 2758
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                              3.4%; Score 160; DB 4; Length 1557;
48.3%; Pred. No. 5e-21;
ative 0; Mismatches 575; Indels 18
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                                                                                      3833 ACTTCA 3838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 554 ATATGCGACTGAGATAAACGACCAATCGCTCGGAAAACCTCTTGCATAGCAGGAGATTCG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          728 GCACCCGTGAA-----AGCACCTTTTTCATGACCAAATAATTCCGTTTCGATTAAATCT 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 788 TCATCAAGGAATAGTGTTCCGCCATTTGCTTGTTCAAAGCGGCCTTGATGTTGGGTGTTT 729
                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTATAATATAAATCCTCACAAAACCTACCAGCTTTACTTCACTTTCAATATCTTTGGAA 2998
                                                                                                                                         TOTTOTTTAAAGGTCTTTTCAAGTACCCATCGCATGGCGCGATCGTCATCAATAACCCAT
                                                                                                                                                                                                                                                                                                  TTTTCATAAGCCATCTTGATCGCGGATAAACCATCAACTGCTAATTTAGTGACATAATTA 3772
                                                                                                                                                                                                                                                                                                                                                        GTTAACCCATCAATA-----CCTGGCATACGAATGTCAGTTAAGATGACATCGGGCGCA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCGCTGTCATAATGATAACAGGCAAGTCGGGGTGAGAGTTTTTCACTTTAGATAAGAAA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGACTATTTCATAATCCTCAA-----ATGCTGATTTCAACTCATCATTTTCTCTACGT 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTATCGTAACGTAAATCTGTTACT 3118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGCCGCGACAATTCTGACATCTACTTTAACGGGTATATGTCCACCAACTCGGTAAAAC 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTGGTATAAGTCTTCACGGAAACGACCTTCATTCACCAGTTTTTCTAAGTCTTGATGG 909
                            ATTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTGGTAAATACTCAAATGCACCAGTCTGATAGCTTGATACAGCAGATTCTAAGTCCGAA 315
                                                                                                                                                                                                                                              TCATGATGTAAACGTTCAAGTGCTGTTTGAGCTTCTTCAAAATTGGTGACGTCAAATCCT 141
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RESULT 3
US-09-107-532A-350
JS-09-107-532A-350
Sequence 350, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stam
APPLICANT: LYNN A DOUCETTE-STAM
APPLICANT: LYNN A DOUCETTE ACI
                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...1071; SEQUENCE DESCRIPTION: SEQ ID NO: 350: US-09-107-532A-350
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Best Local Similarity 49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (781)893-50
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinifello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: CD/RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                       584 PATAATATATATTTTTGACTGGTTTCTTGATATAAATTAGGTAAAAAATGAAAATCAGT 643
                                                                                                                             130 GATGTCCGTATTTGGGGAAATGTACCTGAACAGATTGATGAAATCAATAAGTATCATACA
                                                                                                                                                                                                                                                                                      644 ATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                   504;
                                                                          764 AATTTAAAATATTTACCCACATATCATCTACCAGACACATATATGCAACCAGCAATATA 823
                                                                                                                                                                                704 TCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAA 763
                                                                                                                                                                                                                                      70 GTTCTTGGTCCTGGATCTTGGGGCACTGCTTTAGCACAAACATTGGCAGAAAACGGGCAT 129
                                                                                                                                                                                                                                                                                                                                             10 ACTATAATGGAAATTATCAATTATTTATTTGGAGGAATATCCATGAAACAAAAAATCGCA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1071 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                      AATCAGCATTTTTTACCTGATTTGACGATCCCAGAATCGATTATCGGATATAAAGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 515; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 155; DB 4; Length 1071; Pred. No. 3.9e-20;
                                                                                                                                189
                                                                                                                                                                                                               WS-08-956-171E-513/c
US-08-956-171E-513/c
; Sequence 513, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                 Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1022 AAATCATGT 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1122 ТGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTG 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1062 CAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCAT 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1002 AAATTITACAATATAATCCAATTITTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTG 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1602 ACATATTAT 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1542 TTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAGCCATATCAA 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1482 GAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAA 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1422 AAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGAAG 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1362 TTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAG 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           842 TGTTÄGGÄCÄGGGACATÄÄGCTGGAÄGAÄGTTCTÄGÄÄÄÄÄCÄTGGGAÄTGGTCGTTGÄGG 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               668 TAGGATTCGGAGATGATGCAAAAGCAGCAATCATGACTCGAGGATTGGCAGAAATCAGCC 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        608 TAGAAACTGGTGCAGCACTGAAAAATATCATTGCAATTGGTGCCGGCGCTATCCATGGAT 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 GAA--GAAAAAAGACAGGCAATTGTTGTATTATCTGGTCCTAGCCATGCTGAGGAAGTGG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 AAAGGACTAGAACAAGATACGCATAAACGAATCTCAGAAGTTTTGGCTGAAGAAATTCCA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           942 TAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATAGCAGAAG 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 TCAGTCGCACAGGAACTTATTGGTAAAATGAATACTAAGCCAATCATTATACATGCAAGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    882 TACGCACCATATGTACACAAATACAACACAAACAGCATATGTGTAAAAAATACTCCAATAT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 GCAGAAGCAGTGGATAACGCAGATGCTATTTTATTTGTTGTTCCAACAAAAGCGATTCGT 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGGGACTTGATCGTTACTTGTACAAGTGTTCATTCTCGCAATTGGCGTGCCGGTAACT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTTGGTGTCGCGATGGGT-----GCCAATCCTCTGACATTTATCGGTTTGAGTGGTG 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAA 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACAAAAACTGTTCATGAATGATTATTTCAGGATTTATACAAATAATGATGTGATTGGCG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTACTCAAACAATCTATAATGTTTTGTATAATGGAGAAGATATCAAAAAAAGCAGCAAAAG 1021
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; SEQUENCE DESCRIPTION: SEQ ID NO: 513: US-08-956-171E-513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 513:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 3.2%;
Local Similarity 53.6%;
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:

NAME: MAIK J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                 1442 ATAMATACATTAATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCA 1501
                                                                                                                                                                                                                                                                            1382 TGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAAT 1441
                                                                                                                                                                                                                                                                                                                                                                                       1322 САТТСААТАĢАГСТТСАТАСАТТААТТӨСТССАТСАТСТТССАСАТСТААТАТТААСА 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1082 ATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAAT 1141
                                                        1502 CTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAAT 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1202 AAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAATTTAGGTAATAATGCT 1261
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                                                                                                                                                                                                                         378 TGCACATCAACATTCTCGGAATTTCACATTAGGATATAAACTTGGACAAGGTGAATCA 319
                                                                                                           318 ATGGATCAAGCATTATCTGAAATGAATATGGTTGTTGAAGGTATTTATACAACTAAATCA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AAAGCTGCATTAATGACTCGTGGCTTAGCGGAAATTAGTÄGÄ-----TTAGGTGAAAAG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 AAAAATATCATCGCAGTAGCAAGTGGTATCGTAGCTGGAATTGGCTACGGTGATAATGCA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAGGTGCCGATCCTATGACATTTCTAGGTTTAGGTGGTATCGGTGACTTAATCGTTACT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTATTTGCGTGTGTACACGAATGATGACTTGATTGGTGTTGAACTTGGTGGTGCATTG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Maryland COUNTRY: USA
     GTTTATCATTTÄGCTAÄÄGÄÄAAAAATGTGGÄTATGCCAATTACAAATGCATTATATAGA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 293; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 154.2; DB (
Pred. No. 5.4e-20)
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
                                                                                                                                                                                              Matches 484; Conservative
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1399: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION UNMEER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION UNMEER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMEER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REPERENCE/DOCKET NUMBER: GTC-012

TELEPHONE: (781)893-8277

TELEPHONE: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (B) LOCATION 1...1062 SEQUENCE DESCRIPTION: SEQ ID NO: 1399:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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705 CAGTIAACTIAIGGGGACGIGATCATAGAAATATTACACATATAAACACTIACCGAAAAA 764
                                                                                                                                            645 TITTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATAT 704
                                                                                         56 TTTTAGGACCAGGCTCTTGGGGTACTGCTTTGGCACAAGTCCTCGCCGAAAACGGACATG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1062 base pairs
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                                                                                                                                                                                                                            Score 139.8; DB 4; Length 1062; Pred. No. 2.5e-17;
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AND AMINO ACID SEQUENCES RELATING TO
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                             Sequence 1, Application US/09557884

Patent No. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  1596 TATCAAACATATTAT 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1536 TACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAGCCA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1416 GACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTG 1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647 ACGGCTTAGGGTTTGGCGATAATGCAAAGGCAGCAATCATGACGCGCGGATTAGCTGAGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 AATATGTACAAGAGCTGTTCATGAATAATTATTTTCGGATCTATACCAATCCTGATGTGA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467 AAGTAGCAAAACATGACATCACTACGATCACAGCTGCAAGTACAGATGCAAAAGCAGCAA 526
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                                                                                                                                                                                                                                                                                                                                                                        CAAAAGAAATCATGT 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGCCGTTTAGGTGTAGCAATGGGTGCCA-----ACCCGCTGACCTTTATCGGATTAA 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                              635582 GGCCCAACTTTTGCAAAAGAATTAGCGCAAGGTCTACCATCAGCTATTACGCTTGCTGCC 635641
                                                                                                                                                                                                                      635522 TTACTACAAACCGTAGTTGAAGAACAACTCGGAACGCAATATCCACTAGCTGTACTTTCT
                                                                                                                                                                                                                                                                                                                                           635462 TTAAAAGCCCATCACCGATTAATTTGGGCAACAAAAGGTTTGGAACGTAACACAGGGCGT 635521
                                                                                                                                                                                                                                                                                                                                                                                                                                                               635408 ATCGTGGTGCCAÄGCCATGCTTTCGGTGAAATTCTTATAAAAAT-----CAAACCGCAC 635461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635351 GATCTTCATTTAGAAAGTAATCTTGCACAAGCAAT---GGAATATTCTCAAGATATTTTA 635407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635291 GCACAAATGCAGACAGAACGACAAAATTATCGTTTTTTGCCGGATGTCATCTTTCCTGAG 635350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 635231 ATTACCTTTTCTCGCAATGGTTCTCCCACTCACTTATGGGGGCACAATCCCGCCCATATC 635290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635171 ATAACTTCGCAAACACCAATCACTGTGCTAGGTGCGGGATCTTATGGAACTGCGCTGGCA 635230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 50.4%; Pred. No. 3.1e-16;
1097 GATAATAAAGAACTTG----GTGAATCATTGATAGAAACAATAAGTAATGATGATGTTCTAAAA 1153
                                                                                                                                                           1037 GGTCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGT 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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ADDRESSE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                977 AAATTTCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTATACTCCTCT 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       860 TTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAAACAGCAT 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800 AACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATC 859
                                                                                                                                                                                                                                                                                                                                                                                                  920 ATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAA---ATTACATCACTC 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 АСАСАТАТАААСАСТТАССБАААААТТТААААТТТТАСССАСАТАТСАТСТАССАБАС 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 ATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    620 ATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCA 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/557,884 FILING DATE: 25-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 301-309-8504
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US-09-643-990A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Applicatio Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        635702 GTTTATATAAATTCGGATATGACTGGCGTTCAACTTGGTGGAGCAATTAAAAAATGTGATC 63576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
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                   NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9410 Key West Avenue CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09643990A
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                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
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TELEFAX: 310-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635351 GÄTCTTCÄTTTÄGAAÄĞTÄÄTCTTĞCACÄÄĞCÄAT---GGÄATÄTTCTCAÄGATÄTTTTA 635407
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                             635996 ÁTGGÁAAAÁTÁTÓGGGCÁAGTCGTAGAAGGTTTTTTATAATACAAAAGAAGCCTATTTGCTT 636055
                                                                                                                                                                                                                                                                     635876 ACCAATACATTTATGGGAATGTCTGGATTGGGCGATTTAGTGCTAACTTGCACCGATAAT 63593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635642 AATAACGAGCAATTCGCACGGGAATTTCAGTCTCGTATTCATTGTAGTAAAGGTTTCCGA 63570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635291 GCACAAATGCAGACAGAACGACAAAATTATCGTTTTTTTGCCGGATGTCATCTTTCCTGAG 635350
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                                                                                       1454 ATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTA 1513
                                                                                                                                                                                                                                                                                                                         1334 CTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAA 1393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1097 GATAATAAAGAACTTG----GTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAA 1153
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LENGTH: 1830121 base pairs
                                                                                                                                                                                                        1394 CATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTA 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1274 ATAACTAAAGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGAT 1333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 ACACATATAAACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGAC 799
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Similarity 50.4%;
76; Conservative
                                                                                                                                                    CAATCGCGCAATCGACGTTTTGGATTAATGCTAGGTAAAGGATTAGATGCCCAAATGGCT 635995
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NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1318
LENGTH: 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.8%; Score 134.6; DB 4; Length 999; Best Local Similarity 48.5%; Pred. No. 2.3e-16; Matches 465; Conservative 0; Mismatches 484; Indels 10;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                         1192 AGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAAATTTAGG 1251
                                                                                                                                                                                                                                                                                                               1132 AATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGATTGG 1191
                                                                                                                         543 GGCGGCCTTAÀAAAATATTATTGCTTTTGGGCGCCGGAGCGATTCATGGCTTTAGGCTTTGG 602
                                                                                                                                                                                                                                                      483 GTTTATGAATGATTACTTTAGAATTTATACGAATGATGATGTGATTGGTGTAGAAACAGG 542
                                                                                                                                                                                                                                                                                                                                                                               423 CATTACAACCATTACAGCAGCAAGCGAAAATTTAGCAGACGCTGTGTATGTGCAAGAGTT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 ÁCGGCAAGGGÁTTGTGGTTTTATCTGGTĆCAÁGCCATGCAGAAGÁAGTCGCTGTTCÁTGA 422
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TGATAATGCCAAAGCGGCAATTATGACTCGTGGTTTAGCAGAAATTAGTCGTTTAGGGGT 662
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-300
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 300
SECUENCE: 1097-08-14
NUMBER: 1050-1050
SECUENCE: 1097-08-14
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988 TGAAATAGCAGAAGAAATTTTACAATATAAT---CCAATTTTTATACTCTCTGGTCCAAG 1044
                                                            357 GACTTTTATTCATGTTGCTAAAGGCATTGAAAACGATACATTTAAGCGCGTATCTGAAAT 416
                                                                                                                         928 AAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAG 987
                                                                                                                                                                                         297 ACCTACAAAAGCAATTAGAGAAGTATCAAAAGATATCGATCAATTACTCACATCTAAAAA 356
                                                                                                                                                                                                                                                   868 TCCTACACAACTTACGCACCATATGTACACAAATACAACACAAAAAAATATGTGTAA 927
                                                                                                                                                                                                                                                                                                                   808 TGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTAT 867
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                                                                          NUMBER OF SEQ ID NOS: 98
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10204708 Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                              PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
                                                                                                                                    PRIOR FILING DATE: 2000-09-01
  ORGANISM: Artificial Sequence
                               TYPE: DNA
                                                      LENGTH: 10467
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1181 GTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGA 1240
                                                      1121 TTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGT 1180
                                                                                                                                                              2405 АДАДАТАЛТАССАТТААСАЛТАЛАДАЛАСТАСАДАЛАЛАДАЛАСТАЛАТТТАЛАЛАЛАСТА 2346
                                                                                                                                                                                                                                                                     2464 ATAAAACCAAAAAACGA-ACAACAAAAATAACGCAAATTTCTAACCTTAATAAACTAAAA 2406
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1219 СТСТАССТАТАСААССТССААЛАЛАЛТСТАЛАЛАЛАЛАССАТАЛАТАТАЛАТАТАДТЕТТ 1160
                                                                                                                                                                                    1339 AAATTAAAAATCCTTATAACCAAAACACCATAAAAATÄÄTTAACAAAAATCCTAAAATCC 1280
                                                                                                                                                                                                                                                                                                     2137 ТGCAACAATATGAAGAAGATACAATACACGTCAAATAAATTAAACAAATTTCTAATAATAA 2196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2017 CATAATAAATTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTT 2076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1421 GAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAAACCTAAAGCTTGTTGAA 1480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       АЛЛАЛАЛА САЛТАЛА ССТТАЛАТ ДАЛЛАЛАЛАЛА СТАЛ ССАТАЛА ТССАЛАТАЛАТА 1760
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Sequence 6, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: DLEK, Alexander

APPLICANT: DLEK, Alexander

APPLICANT: DEPENBROCK, Christian

APPLICANT: DERLIN, Kurt

ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

FILE OF INVENTION: by Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT APPLICATION NUMBER: DCT/EP01/03971

PRIOR APPLICATION NUMBER: DCT/EP01/03971

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10032529.7

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US-10-204-708-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.2%; Score 106; DB 4; Length 6669; Best Local Similarity 44.0%; Pred. No. 5.9e-11; Matches 930; Conservative 0; Mismatches 1155; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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6489 АЛЛАЙЛАЛАЛАЙЛАЙЛАЙЛАГССТАЙСТАТАТАЛАЙЛАЙЛАТАТТТТТТСТТССТАСТТАТАЛ 6430
                                                                                                                                                                                     6669 AAAACAACTTAAAAATAAAAAAAAATATATTTTTTTATATATAAACCTTACTAACAAAAATCCC 6610
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5360 CCAATATAAACGAATTCTCTCA-----TTAAATCTTTCCATATTAAATACTCAAAAT 5309
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                                                                                                                                                              5420 TATTACTAACCACTAAAATACCTTAATTATAAACTACTAAAACGTCTTAACTTTTCTCTCA 5361
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// ORGANISM: Acinetobacter baumannii
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                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GATY L. BATEON et al.
APPLICANT: GATY L. BATEON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CUPRENT APPLICATION NUMBER: US/09/328,352
CUPRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 333
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 333, Application US/09328352
Patent No. 6562958
Query Match
Best Local Similarity
                                                                                                                                                       LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>AATTAAAATCAAATTAAAAAATAAATAAAATCAATTCCACAAAACACCTTAAATAAATA</u>
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                              Length 1077;
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RESULT 13
US-10-204-708-23/c
; Sequence 23, Application US/10204708
harant No. 6677731
Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
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CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEG ID NOS: 98
SEO ID NO 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 451; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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                                                           2104 СТААТТАСССАЛАЛАССТТЛАЛАТАСАСАТТССТССАЛСЛАТАТСЛАГАСЛАТАССЛАТАС 2163
                                                                                                                                                                                         2044 ATTTCAAACATAAAATATGATAAACTGTTTTTTATGCCCATTAGTTCTTAATAAAATTG 2103
                                                                                                                                                                                                                                                                                                                              1984 TATTTACTACGTAATATTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACAT 2043
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1924 АЛТТТТАСАТАЛАТААСТААТАЛАААССААССААТАСАТАТТАТТАЛАТТАСТААЛАСАСС 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7746 АТААТААТААТТТАТТААĀĀАТАААЛААЛААĀАСТААЛĀСĀАЛĀААДАСТĀЛĀĀССТĀ 7687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1567 ACATGAGAATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCCT 1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2%;
Similarity 47.2%;
   CTTATTTATAAAATAATATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACAT 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             АТААСТААЛААААЛАСААЛААААТААСССАААААТАТАТАССААЛАААААСААСААААА 7627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCACATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATA 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-73
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PRIOR APPLICATION UNMBER: D2 10019058.8
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                             Query Match 2.2%; Score 104; DB 4; Length 5152; Best Local Similarity 43.9%; Pred. No. 1.3e-10; Matches 987; Conservative 0; Mismatches 1220; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:73
LENGTH: 5152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 73, Application US/10204708
Patent No. 6677731
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: DNA
Artificial Sequence
4735 TOTTCATTATTCAATATTCTCACGAAAAAAACACAATACCTTTTATCCTTTCAAATACC 4676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6974 AATCATACATTTACCGAAAACGATAACTCATACCTATAATCCCAACACTTTAAAA 6920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7093 АААЛАЛААТТСААААЛСАСТТААТАТСТААСДАТААССБААЛААССВААТСТТСТАА 7034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2224 АGTATATCATACCTAAGTAAGATATCCCTACAGCATGTATCAAATAATAATAAAGAAAAATCG 2283
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                                         ACTTTTTAÄAAACAÄATÄTCCTÄATÄTTÄTTÄAAÄCATTTCTTÄAAAAATCCAAÄÄATÄCCT 4556
                                                                                                                                    ACAAAATAATAATACTATCTAATTAATAAAAAAATCCTCAATAGTCTTTAGCAAGAACTA 451
                                                                                                                                                                                 ТАЛАТТТАЛАЛАЛАСАЛАЛСАЛА ----САЛАСАЛАЛАЛАЛАЛАЛАЛАЛССТАЛЛАЛТЛА 7094
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                        1529 GTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGAT 1588
                                                                                                                                                          1410 CT-TTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTA 1468
                                                                                                                                                                                                                                                                                                                                              1350 GTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGG 1409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4317 CCGAÁCATAÁTAACTCATÁCCTATAATCCCAACACTTTAÁAÁÁÁCCGGAÁATAÁATAÁATÁÁÁC 4258
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US-10-204-708-14/c
                                                                                  Patent No. 6677731
GENERAL INFORMATION:
                                                                                                                 Sequence 14, Application US/10204708 Patent No. 6677731
      APPLICANT: OLEK, APPLICANT: PIEPE APPLICANT: BERLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1949 ААБААССААТАСАТАТТАТТАААТТАС-----ТААААСАССТАТТТАСТАСБТААТА 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1889 ACACTTTTTCACTACATCATGTATATAATGAACATAATTTTACATAAAATAACTAATAAA 1948
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                                                                                                                                                                                                                                                                                                                                        2474 GAAACATTACACAATCCAAGAATTTTCA 2501
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                                                                                                                                                                                                                                                                                               2537 TAACAACTACAAAAACCCAAAAATAACA 2510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTTAAAAAGATGACTTCACAATTCATACATAAATAATTATACATGCAATGTTTATTCA 2473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATAAATTTTAAACAACTAAAACTACACCGAAAAAACCTATTCAAAAAAATAATATTTAA 2598
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PIEPENBROCK,
BERLIN, Kurt
                                                            Alexander
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PRICR APPLICATION NUMBER: PCT/EPO1/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-044-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
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SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 948; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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ORGANISM: Artificial Sequence
FEATURE:
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                                                               5470 AATACTAATCAACAATAAAAAAAAACTAACTAATATATACGTAAT-----AAATCTCA 5417
                                                                                                                                                                                    5767 TAAATCCCATTCTCTTAAATACTACGTTATCCAATTTATCTCTCTTTAAATAACAAAAAATA 5708
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                                                                                                                                                                                                                                                                                                                                                                                                                       900 AAATACAACACAAACAGCATATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTA 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 2.2%;
Similarity 43.9%;
                                                                                                                        TCGAAATTACATCACTCAAATTTCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATC 1019
                                                                                                                                                                                                                                                                                                                                                           ACAACAATACATGTATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACAC 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTG 839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAAAAATAACCAAATAAAAATCTCTATAAATTAAATCAAACTAATTT-----TAACAT 5768
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2084 ATTAGTTCTTAATAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAACA 2143
                                                                                                                                             4402 CGCARARARTCACTTARACCTARRARACARARATTACRATRARCCGRARATRACGCCACT 4343
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                                                                                                                                                                                                                                           2026 --TTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCC 2083
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Patent No. 6562,588
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER FILE REFERENCE: GTC99-03PA
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1302
LENGTH: 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3992 ÁAÁTÁTATAAÁAÁTÁAAATÁTTCATÁTTATTÁTTÁATÁAÁCÁTAACTÁTTÁATTTAAA 3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2444 ATAAATAATTATACATGCAATGTTTATTCAGAAACATTACACAACCAATCCAAGAATTTTCAA 2502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4222 TCCATÁAAAACAAÁAACA----TÁAAACÄAÄACTÁAAAAAAACACAAACAAATTATTATA 4167
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  1013 TCCCAATCCATACAAATTTTCTGAATAAAGTGATTGGCTAGTAAAAGGACATCTTCGCCA 954
                                                                                                                                                                                                1133 GCÁTCTTCACTTÁAGGTAÁTTGCGCGCTCAÁTCÁTATTTCTTAATTCGCGAACATTACCC 1074
                                                                                                                                                                                                                                                                                                 1193 AAAGGATTAGAAATATTCGCTCTTAGAGGAGGAGGATGTAAATGAGATACATCTATCGTA 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1313 GCATTGAGTAAAATATCTTTTCAATATTTTCTAAATAACGTTCTAAGCCTTCACTTGGT 1254
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                                             2837 CCTATTTTTTACAGATGCTATTCATAAAATACCTACACAATTCCGGTATATCTGTACAA 2896
                                                                                                                                                                                                                                              2717 TTAGGAGATTTCATAATTAAAATCCATTCTATAACATTACGTAATTGTCTTAAGTTACCT 2776
                                                                                                                                                                                                                                                                                                                                              2657 TCATTAATAGGCGAATTAGATACTATATCTACTGGTAAATCTTTTGCTGTAATCATCTCC 2716
                                                                                                                                                                                                                                                                                                                                                                                              1253 AATTTTTTACGACTTGAGGAGCTGCCACAGTGGTTTGTATGCTTTGAGCAGCCGAAGCA 1194
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                                                                                                                                             GGCCATTCATATGACTGCATTGCTATTAAAGCTTCATCACTTAATACATGAGTACACAAA 2836
                                                                                                GGAAAGTGTTGCTGTAGCAGATAAGTTTTGGCCGCTTCTGTTAATTGTTTAGGTGGCGTT 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 101.4; DB 4; Length 1434;
45.1%; Pred. No. 3.2e-10;
ative 0; Mismatches 611; Indels 18;
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US-10-204-708-11/c
                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/10204708 Patent No. 6677731 GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Disgnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REPERENCE: 5013.1012
CURRENT SOULD NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                     APPLICANT: OLEK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3677 CTTAA 3681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3557 ATATGCAGAGACTTTACAGCAGTGGCAATATTACCATGCCCACTAATCATAATAACAGGC 3616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3497 TTTACAACTAACTTTAATCTTCCTTCTGTAAAAGGCTTTTCTATATAATCATAAGCACCC
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                                                                                                                                                                                                                                                                                                                                     Alexander
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PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
PRIOR DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 690; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3966 AACAACTAAATTATCTATTCCTTAATTCTCTTATCTACAAAATAAAAATACTATTAAAAT 3907
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          2306 AAAATTTCCAACTTCAACAACAAAACTCAAAGTTCTATTATAACAAATTCAAGAATTATA 2365
                                                                             3260 CTTCCATATATACTTATTATAATACTTAATAACCCACCATAATTTTAATATCCTAAAATA 3201
                                                                                                                                                                                                             3440 CCTACTTCCACTAAAAAACTAAATCCCACACTTATTTTAAAAATTTTAAAAATACAATAACT 3381
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Similarity 45.1%; Pred. No. 4.5e-10;
90; Conservative 0; Mismatches 803; Indels 37;
                                                                                                                                          CCACCTACTCT-----AAACATAGGAACCAATAGTATATCATACCTAAGTAAGA 2245
                                                                                                                                                                                                                                                                                                                                                                                                         ТССРАСРАТАТСААСААСАТАСАСТСРАВАТАВАТТАВАСАВАТТСТВАТАТАВА 2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGCCCATTAGTTCTTAATAAATTGCTAATTACCCAAAAAAGGTTAAAAATACACATTCC 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAÁAAÁTTTTAACAÁACACGATTATÁAATATÁÁAÁTCCCACÁTATAÁÁÁTTATATCCT 3441
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                                                                                                                                                                                                                                                                                                                                            ТАТАСТАСТАСААААААĆČĀAĀĆČĀCĀĀĀAAACGTTAĀĀĀATTAACTATTCTAAAAAAAAT 3321
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APPLICANT: DIEFENBROCK, Christian
APPLICANT: PIEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 501.1012
FULE REFERENCE: 501.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
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US-10-204-708-60/c
; Sequence 60, Application US/10204708
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6677731 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 60
LENGTH: 6156
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Best Local Similarity 44.1%;
Matches 1023; Conservative 0
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                                                                                       5358 AAACTTTAAAAAATATATACACTCATAACAATAACGATAAAAACAATCAAATACTAAAA 5299
                                                                                                                                                                                                                                                                                                  5468 ATATATCTATATATATATATAAATATAAACACATACCCAAATCTTATCAAACCCAAAA
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     982 TCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCC 1041
                                                                                                                                                                                                                                               862 AACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACAGCATAT
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Pred. No. 4.9e-10;
0; Mismatches 1260; Indels 36;
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2058 AȚAŢGAŢĄAACŢGŢŢŢŢŢŢŢAŢGCCÇAŢŢĄGŢŢĊŢŢĄAŢAAAATŢGCŢAAŢŢĄCCCAAAA 2117
                                                                                                                                4225 TACTACTAAAATATTATTACAAATATATTTTTATATCAATTAATTAATACACCAACCC 4166
                                                                                                                                                                                                                                                       4285 АТАРААТАСААААТТАТАТТАРААТАТТААСАТААТТТАВАДАТААСААТТАСАРДА 4226
                                                                                                                                                                                                                                                                                                                           1879 ATATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACATAATTTTACATAAAAT 1938
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      TATTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATAAA 2057
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PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR TILING DATE: 2000-06-30
PRIOR TILING DATE: 2000-09-01
NUMBER OF SEC ID NOS: 98
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US-10-204-708-32/c
; Sequence 32, Application US/10204708
; Patent No. 6677731
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Best Local (
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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003.05-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 8093
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                             1631 TAATTTCAACACAATGATAAATAAACGGTCAAAAATATAGAATACAACGTTCACCACATA 1690
                                                                                                                                6716 TÄACCTÄATTCCTTÄAATTTACTAAATTÄATAACCACAAATTAAAATATTTCÄATÄATTA 6657
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      TAÁATTAÁATCCTATTTATAATTTÁATTTTACATÁÁTAAACTTTAAAATTACCTTTTCATA 6537
                                                                                                                                                                                          AGAATATATCACTAGATAAAGCCATATCAAACATATTAT-CTTAGTCTATCATCCTTTGA 1630
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RESULT 20
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: DCT/EP01/03971
PRIOR APPLICATION NUMBER: DCT/EP01/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
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PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DC 10019173.8
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PRIOR APPLICATION NUMBER: DC 10032529.7
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PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DC 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER: DC 5000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 98.8; DB 4; Length 6866; Best Local Similarity 46.8%; Pred. No. 1.3e-09; Matches 453; Conservative 0; Mismatches 502; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6677731
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                       5746 TTATATCTAAATATATCTAAATAAATATATAAAAAATCTACATATATCTAAATCTATATA 5687
                                                                                                                                                                                          1972 ТАСТАЛАСАССТАТТТАСТАССТАЛТАТТАСАТАСАТСАТСТСТСАСАТАЛТАЛАТТСТАТ 2031
                                                                                                                                                                                                                                                                                                                                     5864 TTTCTTTTCGATATTT--CAAACCACAATTAATTAAATCCACAAATACAAAACCCACAA 5807
                                                                                                                                                                                                                                                                                                                                                                                                            1912 ТАТААТGAACATAATTTTACATAAAATAACTAATAAAAAGAACCAATACATATATTAAAT 1971
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CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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SEQ ID NO 80
LENGTH: 8961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 80, Application US/10204708 Patent No. 6677731 GENERAL INFORMATION:
                                                                                                                                    Query Match 2.0%;
Best Local Similarity 44.0%;
                                                                                                                Matches 939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
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                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (5096)
OTHER INFORMATION: n is a or g or c or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5686 AAĀĀTĀAATAAAAĀĀTAAACATĀĀĀĀTCAAĀĀĀĀCTTCTAT-----ĀAAACAAAAAT 5634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2272 AAAGAAAATCGTTATGTATATTATACAATTACAAATTTCCAACTTCAACAACAAAAAC
                      7239 ÁAÁATÁTTÁACTTCTÁTACAAACÁÁÁÁÁÁÁAAATAAÁAÁACATTATACAACTÁAAAATTTT 7180
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                                                                   397 ATAATAGTACTATCTAATTAATAAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAAT 456
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                                                                                                                                    Score 95.8; DB 4; Length 8961; Pred. No. 4.7e-09;
                                                                                                                Indels 42; Gaps
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1522 ACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATC
                                                  6168 ТАССАРААТАСТАСТТТААСССАВАРАВАВЕТТАРАВАТАТАСВРАЛТАРАВАССВРАВАС 6109
                                                                                          1462 CAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAA 1521
                                                                                                                                       1402 CAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCA 1461
                                                                                                                                                                                                                                    6286 CTAAAAAATACCTAAATTTTAATAAAACTAAATAAACCCTAAATAAACTCCCAACCCCC 6227
                                                                                                                                                                                                                                                                                 1342 ATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACG 1401
                                                                                                                                                                                                                                                                                                                                                                           1282 AGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATAC 1341
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  Sequence 3331, Application US/09543681A Patent No. 6605709 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                  5268 TCTCTAACATATATATAAAATATAAAAAAAAACAAAATATATATATATATATATATATATATATA
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Best Local Similarity
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1412 TTTGGACTAGAAATAGGAAAAGGTAGAAATATAAAATACATTAATAGATCACAACCTAAAG 1471
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                                                           ATGGCTGGTTTGGGTGATTTAGTTTTAACCTGTACTGACAACCAATCACGTAATCGTCGC 786
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PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 3331
SEQ ID NO 3331
FINCTH: 1023
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-3331 APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05 2.0%; Score 95.6; DB 4; Length 1023; 47.3%; Pred. No. 3.6e-09; ative 0; Mismatches 494; Indels 21

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CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR TILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
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TYPE: DNA
ORGANISM: Artificial Sequence
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                         1678 CGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGT 1737
                                                                                                                                                                       1923 TÁCACTAAATAATTTTCACAÁÁCTCTÁCAAAÁCÁAAÁÁTAATTÁCCCÁCÁTTTCÁTÁATT 1864
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                                                 2816 CTTAATACATGAGTACACAAACCTATTTTTTACAGATGCTATTCATAAAATACCTACAC 2875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1146 AAĀAĀĀCTĒCATTĒCCAATTĀCĀCGTTĀTĒTTCĀTĀTĒTĀTĒTTĒTTĒCECĀTĀTĒTĀCĀTĀA 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1803 АТАРАРАРАТТАРАСАСАРТАРАВАРАРАТАРТВЕТТАР - АРАСТРОТТЕРАРАВ 1746
                                                                                                                                                                                                                                                                                                                                       2636 ATAACTTTAGCACTTAAAACATCATTAATAGGCGAATTAGATACTATATCTACTGGTAAA 2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2516 GCTGAACGTTCCATTCCAACAAATTCAGCAGTTCGTGATACATTACCTCCAAAACGAGAT 2575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2336 AGTTCTATTATAACAAATTCAAGAATTATATATACTTCACCAACACACATAGTTATCAAATT 2395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1858 СТТТТАСТТАТТТАТАДАДАТААТАТСТТТССАСТСТТТТТСАСТАСАТСАТСТАТАТАТ 1917
  CGTAATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATTGCTATTAAAGCTTCATCA 2815
                                                                                                                                                                                                                                          TCTTTTGCTGTAATCATCTCCTTAGGAGATTTCATAATTAAAATCCATTCTATAACATTA 2755
                                                                                                                                                                                                                                                                                           CTTACTTATTTATTAATCTTTCTTAAATAAATATATAACT--CACATTTACTTCAATA 849
                                                                                                                                                                                                                                                                                                                                                                                           ACTACTAAAATAACTCCCGACACCGTCAACACTAAACTAAAATAACAAATAACCAACTAT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                      AACTGAGTTTTTAAATACTGTCTTTCAAATTCTTCACGAGCTTTTACGTAATGGTACAGAA 2635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTTCTCTTAATACTCCAATTCCCTTCTACATCCCAAAAATATATACAATAAATTTATT 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTACGGTGTAAT 2515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAATATATTTAAATAAAAAAAAATTAAAATCTAAAAACCAACTTAAAAACAAATACTA 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAATACACGTCAAATAAATTAAACAAATTTCTAATATAACCACCTACTCTAAACATAGG
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OY 591 TATAATTTTTGACTGGTTTCTTGATATAATTAGGTAAAAAAATGAAAATCAGTATTTTAG 650 1791 TATTATTTAAAAATTAATTATATATATATATAAAAAAAA	1911 AAAACCATATCAACACTTCCAATAATAATCCTATATTTTACAAATATTTTAAATTCTAAAAAA	411 TAATTAATAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAGACACTT	ON STATISHACTTYPATACTTCTTTAAAACACTCTTTCAAAAAAAAATTAATTA	2.0%; Score 94.6; DB 4; Length 6156;	; ORGANISM: Artificial Sequence ; FEATURE: ; FEATURE: ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-59	6 ID NO	PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: DE 10043826.1 PRIOR FILING DATE: 2000-09-01	APPLICATION N FILING DATE: APPLICATION N FILING DATE:	w w m m	222	PATENT NO. 6677731 GENERAL INFORMATION: APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian	RESULT 24 US-10-204-708-59/c ; Sequence 59, Application US/10204708	608 TATTAAAATCGTA	Db 668 ACTIACTATTTTCGTTAAACACCTACTCTAACAATATTTTATTTTACATACA
2	D Oy	5 A S	Qy Db	D Q	QY Db	80 P	Db Qy	ОУ	dg VQ	Qy db	D Qy	₽ ·Q	D &	9 9
1671 AATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTA 1730	843 ATTCCTÁTCGCTATTACTÁTAÁATÁTÁCACTCTCTTÁÁÁATĆTTCCTTAÁÁATÁT 784 1611 CTTAGTCTATCATCATCATTTCAACACAATGATAAATAAA	1491 CTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCATAT 1550	1431 AAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTA 1490 	1371 TAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAA 1430	1311 TAGCAAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCATGATGTCTTGGAGATC 1370	1251 GTAATAATGCTGTTGCTACTGTTATAACTAAAGGCATGAATGA	1191 GAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAAATTTAG 1250	1131 CAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGATTG 1190	1071 TICCTIGTAGTATAGTACTIGCTGGTGATAATAAAGAACTTGGTGAATCATTGATAGAAA 1130	1011 AATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAGAACATC 1070	951 GTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAATATGCAGAAGAAATTTTAC 1010	891 TATGTACACAAATACAACACAAACAGCATATGTGTAAAAATACTCCAATATTAATTTGTA 950	1556 ATTITCTTCTAAATAAATTATTATCTTTATCTTAACTTTATTCACCTCCCACACAATA 1497	1611 TATATATACAACCCATCCTATATTAATTAATTAAACTAAAATTACATCTATTCAACTAT 1557

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RESULT 25
US-09-543-681A-1742/c
; Sequence 1742, Application US/09543681A
narent No. 6605709
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                                                                                                                                                                                                                                                                                                                                                                                                           US-09-543-681A-1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                        Matches 330;
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1638
TYPE: DNA
ORGANISM: Proteus mirabilis
                                                2847 TACAGATGCTATTCATAAAATACCTACACAATTCCGGTATATCTGTACAATATTCTACTA 2906
                                                                                                     1297 AATGGGTTAATTGCTCCAAAGCATGTGTTTGGAATACAGTCTATTTTTCTATCCATGCGGC 1238
                                                                                                                                                                                                     1357 TTAAAATAACCGCGCGCTCAATAATATTTTCAAGCTCTCGTACATTTTCCCGGCCAAGGAT 1298
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                                                                                                                                                                                                                                                   2727 ТСАТААТТАААНССАТТСТАТААСАТТАССТААТТСТСТААСТТАССТССССАТТСАТ 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2209 ААСАТАББААССААТАБТАТАТСАТАССТААБТАДБАТАТСССТАСАБСАТБТАТСАААТ 2268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1850 AAATTAAACTTTTACTTATTTATAAAATATATGTTTGCACACTTTTTCACTACATCATG 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 ТАТССТТСААЛАТААСАЛААТСССТАССТТААЛААСАТТАААСТСТТААЛАСДАСТАЛАЛ 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 TTCTAÄÄÄCACTAÄTÄÄTÄ 46
     GGGCAATTTTTTGCGTÄÄAAATÄTTTTGCCÄÄTAAGGGGÄTÄTCTTCÄGGTCGCTCCCGTÄ 1178
                                                                                                                                                     ATGACTGCATTGCTATTAAAGCTTCATCACTTAATACATGAGTACAAAACCTATTTTTT 2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATAAATTC 2028
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                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                           2.0%; Score 93.8; DB 4; Length 1638; 46.9%; Pred. No. 8.3e-09;
                                                                                                                                                                                                                                                                                                      0; Mismatches 367; Indels
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                                                                                                                                                                                                                                                      SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57, Application US/10204708 Patent No. 6677731
                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
  Matches 436; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EPO1/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR FILING DATE: 2000-04-06 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR FILING DATE: 2000-06-30
                                                                                                           FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                        LENGTH: 6326
TYPE: DNA
ORGANISM: Artificial Sequence
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h 1.9%; Score 92.2; DB 4; Similarity 44.9%; Pred. No. 2.1e-08; 36; Conservative 0; Mismatches 528;
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US-10-204-708-31/c
Sequence 31, Application US/10204708 Patent No. 6677731
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PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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APPLICANT: OLEK, Alexander
APPLICANT: PIEBENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/BP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
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SEQ ID NO 31
LENGTH: 8093
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45.7%; Pred. No. 2.3e-08;
ative 0; Mismatches 890; Indels
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2236 CTAAGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTAT---- 2291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1389 ААААССАААСТАТААСТААААТТТ--АААТАААТТААТАТСТАААСААТТААААТААА 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1520 AAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATA 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1439 CTTÄAC------TATTÄAÄÄCACCTTAATCTÄTÄÄTTACTAATCCAACAAATTCAA 1390
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                                                                                                                                                                                                                                  2351 AATTCAAGAATTATATATACTTCACCAACACATAGTTATCAAATTCTATAATACATCATA 2410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2176 ТТАРАСАРАТТТСТРАТАТАГАРССИССТРСТОТРАРССИТАВОВАРСЕВИТАВСТРОТАТОВ 2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           696 AAAAACTAAAAACCTAAAAACCACTTCTACTTTCTAACCCCAATTCCTTAAATATTAAA 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       815 АТАЛАСТТАСАТАТСТАЛАЛАЛАСТАСТАТВАТВАЛАЛАЙСССБАЛАЛАЛАЛАЛСТАЛАЛАЛА 756
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                                                                                                                                                576 ACATCATATAATCATTAAATAAAAAAAAAATATAAACCAAAAATTTTAAATTAACCCTTA 517
                                                                                                                                                                                                                                                                                                                              755 TCTACCGATAATTTCCCAATAACTTTAAATATTCACA-ACAAAACTTTATTACTTAAAAA 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 28
US-10-204-708-8/c
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CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR APPLICATION NUMBER: DC 10019058.8
PRIOR APPLICATION NUMBER: DC 10019058.8
PRIOR APPLICATION NUMBER: DC 10019173.8
PRIOR APPLICATION NUMBER: DC 10019173.8
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DC 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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Patent No. 6677731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CLEK,
APPLICANT: PIEPI
APPLICANT: BERL!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication TITLE OF INVENTION: by Assessing DNA Methylation FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 6020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                      3387 ACTITCCACACCTAAATAACAAAAAAACTACTCCCTTTACAAATCCTCTTCCCTTTTCCGC 3328
                                                                                                                                                                                                                                                                                                                                                    3447 САЛАДАЙССТАЛАЙСТАЛАТАЛАТТАЙСТТССТАЙЙАСТАЙЙТСЙАЛАЙЛАЛАЛАССССЙ ЗЗВВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                2471 TCAGAAACATTACACAATCCAAGAATTTTCAATTTA 2506
836 TCTGACAATACATGTATTATCTTAACTATTCCTACACAACAATTACGCACCATATGT 895
                                                                                                                     776 TTACCCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTA 835
                                                                                                                                                                                                                                                                                                                                                                                                 596 TITTTGACTGGTTTCTTGATATAAATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 ATTAATATATTTCAAATTTATTATACTACTCATCATATTTAGCATAATATCACATCTGAC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 AATAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAGACACTTAACTT 475
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                                                                                                                                                                  TGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAAAATTTAAAATAT 775
                                                                                                                                                                                                                                                                                                       GGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTA 715
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                                                        1912 ТАТААТGААСАТААТТ----ТТАСАТААААТААСТААТАААААДАGAAССААТАСАТАТАТ 1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1376 TTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGT 1435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2617 СССТАТААСТССААСАСТТТААЛАЛАТСGЛАЛТТАЛЛАЛАЛАТАЛСТТАЛАСТТАЛАТТТТ 2558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1436 АGAAATA--ТАААТАСАТТААТАGАТСАСААССТАААGCTTGTTGAAGGAACCAGTACTG 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTATGTAACATATTACATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATAT 1791
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                                                                                                                       AAAATAAACTAAAACATACATAACAAAATAAATTTAAAAATTTCGAAACGATTAAA
                                                                                                                                                                               ATTAAACTTTTACTTATTTATAAAATAATATGTTTGCACACTTTTTCACTACATCATGTA 1911
                                                                                                                                                                                                                                                 CTATCAAATTTTCAAAATATTTCATTCAAAAAAAAACTCCCCTCTTACTATCCCAATAAAA 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATACAACGTTCACCACATATATAAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAA 1731
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TTŤTÁAAAAACTTÄŤŤTATAAŤŤÁACAÀÁÁÁŤTÁČCAÁŤÁTÁÁÁATCAAÁTTÁTÁAAŤCA 2080
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// ORGANISM: Acinetobacter baumannii
US-09-328-352-3585

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Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 3585
LENGTH: 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
   2917 TCTAATTGGAAGGACATTTAATCTATAATATAAATCCTCACAAAACCTACCAGCTTTTAC 2976
                                                                                                                                                                                      1008 AACTTGCATCGCTTTTTGATTGACATGTCGAGGCATTGTATCGAGTTGGGTTGAGCTCTC 949
                                                                                                                                                                                                                                                 2797 TGCTATTAAAGCTTCATCACTTAATACATGAGTACACAAACCTATTTTTTTACAGATGCT 2856
                                                                                                                                                                                                                                                                                                                                                                                                                                 1128 TAATAGCTCATTGGGTAAGTCTTCGACTTCAATTTCATCTTTACCATTTTGCCATGGTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1967 TAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATAAAT 2026
                                                           ATTCATAAAATACCTACACAATTCCGGTATATCTGTACAATATTCTACTAAAGACGGTAC 2916
                                                                                                                                                                                                                                                                                                      AGCATAAAGCAGAGTGTTTTTAAGCTCACGAACATTTCCTGGCCAGTCATAATTCAATAA 1009
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                                                                                                                                                                                                                                                                                                                                                                  AATCCATTCTATAACATTACGTAATTGTCTTAAGTTACCTGGCCATTCATATGACTGCAT 2796
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ilarity 46.2%;
Conservative
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Pred. No. 3.4e-08;
0; Mismatches 391; Indels 6
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DC 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DC 10019173.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10039529.7
PRIOR APPLICATION NUMBER: DE 10039529.7
PRIOR APPLICATION NUMBER: DE 10039529.7
PRIOR APPLICATION NUMBER: DE 10039529.7
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                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-50
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                                                Query Match 1.9%; Score 89.8; DB 4; Length 6 Best Local Similarity 44.3%; Pred. No. 5.7e-08; Matches 583; Conservative 0; Mismatches 722; Indels
                                                                                                                                                                                                                                                                               SEQ ID NO 50
LENGTH: 6306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/10204708 Patent No. 6677731
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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     1148 CTAMAMATAATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAMAGAAC 1207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3037 CTTACTATTTTCCCTATATATTTTTCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGT 3096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 TTCGCCGCGGACAAGCACTGGAAACTCAGTAATTGCCACTCTTTGAATAATTGAAAACAT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648 CACGCCTTTAT-----GGTCGCGAATTGCTCCCGTAAAAGCACCTTTCACATGCCCAAA
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                                                                                                      Length 6306;
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2224 AGTATATCATACCTAAGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAAAAATCG 2283
                                                                        5198 AAAAAAAACGAAAAAATAAACCAAAAAACAACACTTATACCATTACAATATCTCACT
                                                                                                                           2166 GTCAAATAAATTAAACAAATTTCTAATATAAC--CACCTACTCTAAACATAGGAACCAAT 2223
                                                                                                                                                                            5558 AATCCATAAAATAAAATTAACTCCACACATATCTATAAACTTAAAATAACAAATAAAAAT 5499
                                                                                                                                                                                                                            2106 ААТТАСССАЛАЛАGGTTAAAATACACATTCCTGCAACAATATGAAGAAGATACAATACAC 2165
                                                                                                                                                                                                                                                                             2046 TTCAAACATAAAATATGATAAACTGTTTTTTATGCCCATTAGTTCTTAATAAAATTGCT 2105
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                                                                                                                                                                                                                                                                                                                                                                                                                              TTTACTACGTAATATTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACATAT 2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ТТАРАРА СТТАТСТВА СВАСАТА САТА АВРАНТАВАТ ТСТВА АТА АССВАСТАТТАВАТА 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ТТТТАСАТАРАРАТАРСТРАТАРАДАРАССРАТАСАТАТТАРАЛТТАСТАРАДАСАССТА 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATTA 1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTTAATCAAAATTCCAACAATTTTTCCTAAAAATTCATAAACTACATTCTATACAA 5676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCATTAGCAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATT 1566
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APPLICANT: DIERNANCK; Christian APPLICANT: BERLIN, KIRT ITTIE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication ITTIE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication ITTIE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication ITTIE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication ITTIE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication ITTIE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication ITTIE OF INVENTION: Diagnosis of DNA Replication ITTIE OF DNA DATE: DNA OF DOISONS. PRICE PRILING DATE: 2000-04-06 00109173.8 PRICE PRILING DATE: 2000-04-06 00109173.8 PRICE PRILING DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRILING DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE PRICE DATE: 2000-05-01 PRICE PRICE DATE: 2000-05-01 PRICE PRI	7 31 -204-708-10/c -204-708-10/c uence 10, Application U ent No. 6677731 ERAL INFORMATION:	Db 5018 TAAAATCACGACAAAAAACACTTCATATCATACATAAAAAAAA	5138 AATAAAAAACTCTTAAAAAATCAATAAAAAAAAAAAAA
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PRIOR APPLICATION NUMBER: PCT/EPO1/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 38
SEQ ID NO 38
LENGTH: 5501
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; Sequence 38, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003:05-06
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3164 TAAATAAAAACATATTTTAATACTACATCCTAAAAAAATCACCCTCTATTTÄAÄAAÄTAT 3105
                                                                                               3224 АТАРАССАСТАСGCCCGCCAPAPACTTAAATTTTATCCTAAATACAATAAAAAATATA 3165
                                                                                                                                                                                                  3284 AAACTCCTAACCTCAAATAATCCGCCTACCTCAACCTCCCAAAATACTAAAATTACAAAT 3225
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                                           650 GGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTT 709
                                                                                                                                                 590 ATATAATTTTTGACTGGTTTCTTGATATAAATTAGGTAAAAAATGAAAATCAGTATTTTA 649
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PIEPENBROCK, Christian
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                   2108 AÄACCGAAATCGTÄCCATTACACTCTAACCTACGAAACAAÄÄÄTAAAACTCTATCTCAAA 2049
                                                              1730 AAGTATGTAACATATTACATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTAT 1789
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US-10-204-708-12/c
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                                                                                                                                                                                                                                                               FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-04
PRIOR APPLICATION 2003-05-04
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
TITLE OF INVENTION:
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
                                                                                                                              PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR FILING DATE: 2000-04-06 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07
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PRIOR FILING DATE: 2001-04-06
                                                                           APPLICATION NUMBER: DE 10032529.7 FILING DATE: 2000-06-30
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-12
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LENGTH: 6317
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3474 AÁAAATCTAÁÁACÁAÁATÁTTCTTTAAAATÁÁTTTCAAÁATTTACAAATTTTAAATTATA
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                                                     1008 TACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAGAAC 1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 AGTTCTTTATTCGACATACATATTAAAATCAATCAAAACAAAATAATAGTACTATCTAAT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          653 GCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACAT-----GGTATATCAG 707
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                                                                                                          AAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGA 1187
                                                                                                                                                                TAAAATATTTACCCACATATCATCTACCAGACAGACATATATGCAACCAGCAATATAGACG 827
                                                                                                                                                                                                                ATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAGAACTTGGTGAATCATTGATAG 1127
                                                                                                                                                                                                                                                                                                                                                                                                                          GTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAATAGCAGAAGAAATTT 1007
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                                                                                                                                                                                                                                                                  TCTATTTTCTTTAAAACAATTAATCCTCAACGCCCTCTATAACCTACTTTCTACAACAAC 2941
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1533 AACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAG 1592
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                                                                                                                                  1809 TTCAATTATTTTCAAAAATAATAATTAAATAAACTA-AACGTAACTAACGAATCTACATT 1751
                                                                                                                                                                                                              2192 ТАТААССАССТАСТСТАЛАСАТАББААССАЛТАБТАТАТСАТАССТАЛБТАЛБАТАТССС 2251
                                                                                                                                                                                                                                                                                                                                                                                     1924 CATACTTAAATAATAATTTÄCGTÄÄÄTCATTTÄTTÄACAATÄCÄTCATAAAA----- 1870
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APPLICANT: BERLIN, NOTE

ITTLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

ITITLE OF INVENTION: by Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2003-05-06

FRIOR APPLICATION NUMBER: PCT/EP01/03971

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: DE 1019058.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-04-07

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SEQ ID NO 36
LENGTH: 9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.9%; Score 88.2; DB 4; Length 9347; Best Local Similarity 42.6%; Pred. No. 1.2e-07; Matches 918; Conservative 0; Mismatches 1213; Indels 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                               8454 TCACACCTATAATCCCAACACTTTAAAAAAACCAAAAACAAAAATTACTTAAACCCAAAA 8395
                                                                                                                                                                                     8514 ATATAAAATAACTTTAAAAATTTAAAATTACCTAAAAACTAAACCAAACACAATAAC 8455
                                                                                                                                                                                                                                                                                            8634 CCTAAAAAATAAAAAAATATACCAAAATCCTATTTAAAATACTTAAAATATTCATTTCT 8575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8694 САЛДАДСАЛДАТСТАТАТАЛАДАДАДАСТАТАЛАДТТАЛАТТАЛТАДАСАДАДА САЛДАДА 8635
696 ATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTT 755
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                                                                                                                               636 AAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCAC 695
                                                                                                                                                                                                                                                                                                                                               516 AGCATAATATCACATCTGACATGATTAACAATAGTAACACATTTCTTAACACTAGATAAT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATACAATAAATAATATAATTTTTTGACTGGTTTCTTGATATAAATTAGGTAAAAAATGA 635
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                                                                        1772 ААТТТССТАССТААТТАТАТАААСААНТТССТАТСТСТАТСТСАНТТААССААТТСТТА 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1592 GCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTCAACACAATGATAAA 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1532 GAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAA 1591
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816 GCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACAC
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                                                                                                                                                             ATTAATTCGAAAACAATAAATAAAACGATAAAAACCTAATAAACGTAAAACCACCATTT 7325
                                                                                                                                                                                                                                              CATCGTTAACATCCAACTAAGTATGTAACATATTACATAACAAACTTAAGTATAACTTAA 1771
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                                                                                      2430 TICACAATICATACATAAATAATTATACATGCAATGTTTATTCAGAAACATTA 2482
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US-10-204-708-35/c

Sequence 35, Application US/10204708

Patent NO. 6677721

GENERAL INFORMATION:
APPLICANT: OLEX, Alexander
APPLICANT: DIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt

ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE; 5013-1012

CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR APPLICATION NUMBER: DCT/EP01/03971
PRIOR APPLICATION NUMBER: DCT/EP01/03971
PRIOR APPLICATION NUMBER: DCT/EP01/03971
PRIOR APPLICATION NUMBER: DCT/EP01/03971
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DCT/EP01/03971
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, OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-35
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                                            GACATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCATTAGTTCTTAATAA 2098
                                                                                            ACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATAAATTCTATCATCCTT 2038
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                                                                                                                                                                             ) OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-22
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PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 98
SEQ ID NO 22
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                                                                                       Matches 445; Conservative
                                                                                                          Query Match
Best Local Similarity
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APPLICANT: PIEPERNROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
ITTLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
CURRENT FILING DATE: 2003-05-06
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                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                        LENGTH: 11049
  1530 TAGAACTACCAATTTGCATATCTATTTACAATTTACATGAGAATATATCACTAGATA 1589
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                                                                                   . 1.8%; Score 86.2; DB 4; Length 11049; 45.9%; Pred. No. 2.9e-07; ative 0; Mismatches 513; Indels 11;
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US-10-204-708-26/c
; Sequence 26, Application US/10204708
; Patent No. 6677731
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GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, CI
APPLICANT: BERLIN, Kurt
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PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 26
SEQ ID NO 26
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ORGANISM: Artificial Sequence
FEATURE:
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     2077 TATGCCCATTAGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCC 2136
                                                    5995 АСАСТТАСАНТАВАЛАВАКСАЛАГТАЛТАЛТАЛАСАЛАЛТАТСТВАТТАЛАЛАССАЛС 5936
                                                                                                                                                                                                                                                 6054 CAAATAC-TAAAAAATAAAAACTACATCATTTCTTTTATATACATTTCACAAACGAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6286 АЛАСАЛАЛАЛАЛАЛАЛАТТАЛАЛТСАСАТАСАСАТАЛАЛАТТАСАЛАЛАТАТТСАСАЛАЛ 6227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 2017 CATAATAAATTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTT 2076
                                                                                                                                                                                                                                                                                                                                                  CCTAGCTAATTATATAAACAAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGA 1836
                                                                                                                                                                                                     ATACATATATTAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGA 2016
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45.0%; Pred. No. 2.9e-07;
ative 0; Mismatches 585; Indels
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Query Match 1.8%; Score 84.8; DB 4; Length 6040; Best Local Similarity 44.7%; Pred. No. 4.7e-07; Matches 629; Conservative 0; Mismatches 757; Indels 20; Gaps 7; Qy 1107 AACTTGGTGAATCATTGATAGAAACAATAAGTATGATGTTCTAAAAATAATAATAACCATC 1166	Ar ORM -70	NO 70 CH: 6040	PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: DE 10043826.1 PRIOR APPLICATION NUMBER: DE 10043826.1	PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR FILING DATE: 2000-04-06 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07	ENT APPLICATION AP	BERLIN, Kurt NVENTION: Diagn NVENTION: by A ENCE: 5013 1012	0. 6677731 INFORMATION: NT: OLEK, Alexand NT: PIEPENBROCK.	RESULT 38 US-10-204-708-70/c . Seminarce 70 Application US/10204708	Qy 2496 TTTTCAAT 2503 Db 5458 AAATCAAT 5451	Oy 2437 TTCATACATAATAATT-ATACATGCAATGTTTATTCAGAACATTACACAATCCAAGAA 2495	QY 2377 AACACATAGTTATCAAATTCTATAATACATCCTTTTTAAAAAGATGACTTCACAA 2436	Qy 2317 CTICAACAACAACTCAAAGTICTATTATAACAAATICAAGAATTATATATATACTTCACC 2376	Qy 2257 CATGTATCAAATAATAAAAAAATCGTTATGTATATTTATACAATTACAAAATTTCCAA 2316	QY 2197 CCACCTACTCTAAACATAGGAACCAATAGTATATCATACCTAAGGATATCCCTACAG 2256 Db 5758 TTTTTTTTCAAAAAATTTTTACGATAACAAAAAAAAAAA	QY 2137 TGCAACAATATGAAGAAGATACAAGTCAATACACGTCAAATAAACAAATTTAAACAAATATATAA 2196	Db
Q	Q	ДУ	Db Qy	Db Db	Qy Db	dg Qy	dg VQ	Qy db	Qy db	Qy	Qy	da VQ	4d 6y	Qy Db	Qy Db	Db
2174TCTCAACTACCATCTTCCCACCAAATAATAAATTCGTCCAAAAAAAA	2057 AATATGATAAACTGTTTTTTATGCCCATTAGTTCTTAATAAAATTGCTAATTACCCAAA 2116	2000 TTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATAA 2056	1940 ACTAATAAAAGAACCAATACATATATATATATACTAAAACACCTATTTACTAC	1886 TGCACACTTTTTCACTACATCATGTATATAATGAACATAATTTTACATAAAATA 1939	1827 TGTTATCAGATTATAAATAAGT-CAAATTAAACTTTTACTTATTATAAAATAATATGTT 1885	1767 CTIAAAATTTCCTAGCTAATTATATAAACAAATTCCTATCTCCTATCTCAATTAACCAAT 1826	1707 ATACCCATCGTTAACATCCAACTAAGTATGTAACATATTACATAACCAAACTTAAGTATAA 1766	1647 ATAAATAAACGGTCAAAAATATAGAATACAACGTTCACCACATATATAAAAAGCAGTCAA: 1706 	1587 ATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTTCCAACACAATG 1646	1527 ATGTAGAACTACCAATTTGCATATCTATTTACAATTTACATGAGAATATATCACTAG 1586	1467 TAAAGCTIGTIGAAGGAACCAGIACIGIAAAACCACIGATATCAITAGCAAAAAAACTIA 1526	1407 TGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACC 1466	1347 TTGGTCCATGTCTTGGAGATCTAATATTAACATGTACAACAGAAACATTCACGCAATA 1406	1287 TGANIGAANTTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAA 1346	1227 GANTAATCGCTGGAAAAANTTTAGGTAATAATGCTGTTGCTGCTGTTATAACTAAAGGCA 1286	3133 AAATCAAAAAATCGAAACCATCTTAACCAACATAATAAAAACCTCGTCTCTACTAAAAATA 3074

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RESULT 39
US-10-204-708-19/c
; Sequence 19, Application US/10204708
parent No. 6677731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR FILLING DATE: 2000-04-06 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR FILING DATE: 2000-06-30
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PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6866
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
- 1099 TAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGATGTTCTAAAAATAAT 1158
                                                                                 3485 ТАССААТАЛАЛАЛААТАЛАЛАТАСЛАЛАЛАТТАТАТАТАСТТАЛАСЛАЛААССАСБАЛЛАС 3426
                                                                                                                                                                                                                                                                                             1041 CAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGA-- 1098
                                                                                                                                                                                                                                                                                                                                                                                                     3665 TAACCGTTTCCAAAAAAATCTATTCCTCTACCTCTTTACTACTTAATCTAATATTTTACT 3606
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                                                                                                                                                                                                                                          981 TTCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATACCAATTTTTATACTCCTGGTC 1040
                                                                                                                                                                                                                                                                                                                                                921 TGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAAT 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                     861 TAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACAGCATA 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 1.8%; Score 84.8; DB 4; Similarity 43.8%; Pred. No. 4.8e-07; 04; Conservative 0; Mismatches 882;
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        2350 TTCTÁATÁAAAÁACTTATATÁTÁAAÁAATÁ-----TATÁTTCÁTTATÁTCATTATATAAAC 2296
                                                        2171 ATAAATTAAACAAATTTCTAATATAACCACCTACTCTAAACATAGGAACCAATAGTATAT 2230
                                                                                                              2410 TCAAACACTACTCTAAAACTCTAAAAACTTACTAATAAACAAAAACGAACATAAAACTTATA
                                                                                                                                                              2111 CCCAAAAAGGTTAAAATACACATTCCTGCAACAATATGAAGAAGATACAATACACGTCAA 2170
                                                                                                                                                                                                                2470 АТАТАТАЛАТАСАТАТАСАСАТАСААТСАТСТААТАЛАТАТТТАТАЛАЛАСАСССААТАТА 2411
                                                                                                                                                                                                                                                                   2051 ACATAAAATATGATAAACTGTTTTTTTATGCCCATTAGTTCTTAATAAAATTGCTAATTA 2110
                                                                                                                                                                                                                                                                                                                      2530 АТАСАНТААААСААТСТТТТТАААААССАТТААТСААТСТАСАСААААТТТТТАААТАС 2471
                                                                                                                                                                                                                                                                                                                                                                         1995 TAATATTACATAGATGTCCTGACATAATAAATTCTATCATCCTTGACATATTTCAA---- 2050
                                                                                                                                                                                                                                                                                                                                                                                                                               1935 АЛАТЛАСТАЛТАЛАЛАБЛАССАЛТАСАТАТАТТАЛАТТКСТАЛАЛАСАССТАТТТАСТАСС 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1637 CAACAATGATAAATAAACGGTCAAAAATATAGAATACAACGTTCACCACATATATAAA 1696
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QY 269 GGTCTCTEACATAAGAAACTATTCAAAGAATACCTCTTTCTCTCTTTCTCCATCCA	1051; Conservative 0; Mismatch 149 CTCCACATTGATATCTAGAAGCAAACCATTT	OGGAISM: Artificial Sequence; COTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-29 Query Match Dest Local Similarity 44.6%; Pred. No. 5.1e-07;	. H . W	CURRENT APPLICATION NUMBER: US/10/204,708 CURRENT FILING DATE: 2003-05-06 PRIOR APPLICATION NUMBER: PCT/8P01/03971 PRIOR FILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR APPLICATION NUMBER: DE 10019173.8	4осточние	Db 2175 CAATATATTATTATATACTAAAAAAAACAATTACAAAACAATTACAATAAT	OY 2231 CATACCTAAGTAAGTATCCCTACAGCATGATTAATAAGAAAATGGTTATGTA 2290 Db 2295 TATTATTATTCTTAAATATTTCCCCTAAATATCCAAAAATAAAAAA
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134 CTICATACAT:	14 GCAATTGCATGTGGAATAATCGCTGGAAAAAATTTAGGTAATAATGCTGTTGCTACTGTT	1095 GIGATAATAAAGAACTIGGTGAATCATIGATAGAAACAATAAGTAAGATGTTCTAAAAA 1154	982 TCCCAGTGAAATAGCAGAAGAATTTTACAATATAATCCAATTTTTATACTCT 1034	863 ACTATTCCTACACAACAATTACGCACCATA-TGTACACAAATACAACAGCATAT 921	688 GTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATA-GAAATATTACACATA 746	2019 ATAAATAACTAAATATATTAATTTCTAATATAATAAACATCAATAACTAAATA 1960 628 AAAAAATGAAAATCAGTATTTTAGGTGCAGGATCAGTTTGGCACTAGCAATTGCACT 687 628 AAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACT 687 1959 CCTACATACACATTTCTTTAAAATCTTCAATAATTTTTAAAAAA	448 ACTACAAATATAATGAGACACTTAACTTATTAATATTATTATTATTATTATTATTACTAC

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2325 ACAAAACTCAA-AGTTCTATTATAACAAATTCAAGAATTATATATATACTTCACCAACACAT 2383
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                                                                               2444 ATAATAATTATACATGCA 2462
                                                                                                                                                                                                                                                         2384 АСПТАТСАРАТТСТАТРАТАСАТСАТАТССТТТТАРАРАНСЯТСАСТТСАСВАТТСАТАС 2443
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102 ATAAATTCTTCAAAAATCA 84
                                                                                                                                                                    222 ACCAATATCAATAATAAAATAAAAAATACCACAACAACATCGCAACCATTAAAAAATA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 АСТАЙАСССАЙАЙЛАКАЛАЙАЛАЙЙАЙАЙАЙАЛАЙТТАЙАЙСТТАЙАЙСАЙЙАТСЙАТАЙА 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 ANACHAACTTCAAATCAATATTCTAAATTATCACTTCANAAAACTATACAAAAATAACAA 403
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ALIGNMENTS

US-10-081-051-52 RESULT 1

GENERAL INFORMATION:

Anthony F.

Sequence 52, Application US/100 Publication No. US20030044422A1

Application US/10081051

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APPLICANT: Whitmire, William M.
APPLICANT: Kamper, Sondra M.
APPLICANT: Simbi Bigboy H.
APPLICANT: Simbi, Bigboy H.
APPLICANT: Ganta, Roman R.
APPLICANT: Moreland, Annie L.
APPLICANT: Mwangi, Duncan M.
APPLICANT: McGuire, Travis C.
APPLICANT: McGuire, Travis C.
APPLICANT: NCGUIRE, Travis C.
APPLICANT: NCGUIRE, Travis C.
APPLICANT: NCGUIRE, Travis C.
APPLICANT: NCGUIRE, DUNCAN M.
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: UP-299XC1
CURRENT APPLICATION NUMBER: US/10/081,051
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/269,944
PRIOR APPLICATION NUMBER: US 60/269,944
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Best Local Similarity
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                                                                      100.0%; Score 4750; DB 14; Length 4750; 100.0%; Pred. No. 0; ative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                             0; Indels 0; Gaps
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QY 1141 TGATGTTCTAAAAATATTATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATT 1200	2161	2101	2041	1 1 1 1 9 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1921	1861	1801	1741	1 16 8 1	16621	1 5 61	1501	1441	1381	1321	1261	1201
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Db Qy	D Qy	D Qy	g Q	Qy Db	D Qy	Qy Db	Qy dg	g Qy	g Q	d dd	Qy Db	d VQ	D Qy	Qy	dg VQ	DР	Qy Db
3301 TATTAGCCTAGCAACTACTTCCTTTCCAACACCTGGCGAACCAGTAATGAGTATACGACT 3360	3241 TGGTAGCATAGATGAGTACATAGATATAAATGGAGTATCATACCCCTTGGATTTTTTATG 3300	3181 ATGAGACAATATATTACTTTCCTCACTACCAAATATATTAACCAAGTAATTATTAGC 3240	3121 ATCTATAAAGAACGTACCATGATTTGCTTGCTCTATAATTCCAATATGAGGAGGTACTCT 3180	3061 TCCCTCCTGTAATAATCTGAGTAATCTTAATTGCGTATCGTATCGTAAATCTGTTACTTC 3120	TAACAGGAATCTTACTATTTTCCCTATAI	2941 ATAATATAAATCCTCACAAAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGA 3000	2881 CGGTATATCTGTACAATATTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCT 2940	2821 TACATGAGTACACAAACCTATTTTTTTACAGATGCTATTCATAAAATACCTACACAATTC 2880	AGTTACCTGGCCATTCATATGACTGCATTGCTATTAAAGCTTCAT 	2701 TGCTGTAATCATCTCCTTAGGAGATTTCATAATATAAAATCCATTCTATAACATTACGTAA 2760	Taaaacatcattaataggcgaattagatactatatctactggtaaat	581 AGTTTTAAATACTGTCTTTCAAATTCTTCACGAGCTTTACGTAATGGTACAGAAATAAC 26	2521 ACGTTCCATTCCAACAAATTCAGCAGTTCGTGATACATTACCTCCAAAACGAGATAACTG 2580	2461 CAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTTACGGTGTAATGCTGA 2520	2401 ATACATCATATCCTTTTTAAAAAGATGACTTCACAATTCATACATA	2341 TATTATAACAAATTCAAGAATTATATATATATCTTCACCAACACATAGTTATCAAATTCTATA 2400	2281 TCGTTATGTATATATACAATTACAAAATTTCCAACTTCAACAAAAACTCAAAGTTC 2340
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		9 6 6				4021 TATRAAAATTAGTTACTATTATTACTAATTTATCAAGCATAGGTTTCCTATATATCT 											

8	Db Qy	g &	Mat See Que	US-10		SEQ			יי ספק פ		GEN ; GEN ;	RESULT	ß 8	B &	Ag Ag	do dy	B & B	2
2587 TAAATACTGTCTTTCAAATTCTTCACGAGCTTTACGTAATGGTACAGAAATAACTTTAGC 2646	2527 CATTCCAACAAATTCAGCAGTTCGTGATACATTACCTCCAAAACGAGATAACTGAGTTTT 2586	2467 TTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTACGGTGTAATGCTGAACGTTC 2526	Query Match 29.8%; Score 1416; DB 14; Length 1416; Best Local Similarity 100.0%; Pred. No. 4.6e-215; Matches 1416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium) FEATURE: NAME/KEY: misc_feature TORATTON: (1) - [1416]	TWARE: Pate ID NO 56 NGTH: 1416	CURRENT FILING DATE: 2002-02-20 PRIOR APPLICATION NUMBER: US 60/269,944 PRIOR FILING DATE: 2001-02-20 NUMBER OF SECTION NO.S. 117	TTE OF INVENTION: Ehrlichia Ruminantium Polypeptides, Antigens, Polynucleotides, an ITLE OF INVENTION: Methods of Use TERRETENCE: UF-299XC1 TERRETERENCE: UF-299XC1	PPLICANT: Moreland, Annie L. PPLICANT: Mwangi, Duncan M. PPLICANT: McGuire, Travis C. PPLICANT: McGuire, Travis C.	APPLICANT: Whitmire, William M. APPLICANT: Whitmire, William M. APPLICANT: Kamper, Sondra M. APPLICANT: Simbl, Bigboy H. APPLICANT: Simbl, Bigboy H.	Quence 56, Application US/10081051 plication No. US20030044422A1 ERRAL INFORMATION:	1 0 0 1 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 1 0 1	4741 CTAATTGATC 4750 4741 CTAATTGATC 4750	4681 CAGAACTTACATATTCATTACCATCAATCAATATTTTATCAACAGTAAATCCACAATTGA 4740	4621 TCAAATCAGCCAAAGGCACAAAAAGATAGACCTTGCATCAACAAGTTTACGTATTTCAT 4680	4561 GTAACAGCCTCTTAACTGAGGCATITTTGATCCATGGATGACTGACTCTATTTTGTTTC 4620	4441 CCCGIAIATIACAATTATCAACAATAATAATAIGTCCAAAACTATCAATGAIGAATTTTTGT 4500 4501 TATCATGATACCAATTTGCAAAAGCAGAATATTCTTGAACTGTTATCTGTAAAGTATTTG 4560	
₽ \$	P &) B B	\$ \$ \$	B 8	d dy	B &	р У	B 8	B &	8 8	B &	B 6	DP .	B 2	S B 8	5 B 2	γ δ δ	B
CCAT 12	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1 ATAAGCACCCATATGCAGAGACTTTACAGCAGTGGCAATATTACCATGCCACTAATCAT 1 ATAAGCACCCATATGAGCAGTAGACTTTACAGCAGTGGCAATATTACCATGCAGTAATCAT 3	TALAGO LUCITACAGUTAGUTTAGUTTAGUTTGGGAATATTAGGGCTTTTCTATAATATCI 108 TATAGGTCTCTTTACAACTTTAATCTTCCTTCTGTAAAAAGGCTTTTCTATAATAATC 108 TATAGGTCTCTTTAGAGTGAGTTTAATCTTTCCTTCTTAAAAAGGCTTTTCTATAATAATC 108	1 12 -1	3367 AGTAGCTGCTTTATTAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTAT 3426	3307 CCTAGCAACTACTTCCTTTCCAACACCTGGCGAACCAGTAATGAGTATACGACTCGATGT 3366	3247 CATAGATGAGTACATAGATATAAATGGAGTATCATACCCCTTGGATTTTTTATGTATTAG 3306	3187 CAATATTATTACTITCCTCACTACCAAATATATTAACCAAGTAATTATTATGCTGGTAG 3246 	3127 AAATAACGTACCATGATTTGCTTGCTCTATAATTCCAATATGAGGAGGTACTCTATGAGA 3186	3067 CTGTAATAATCTGAGTAATCTTAATTGCGTATCGTATCG	3007 AATAATTCTCACATCTATACTAACAGGAATCTTACTATTTTTCCCTATATATTTTTCCCTC 3066	2947 TAAATCCTCACAAAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGAGAGACAC 3006		ACTACACAAACCTATTTTTTTACAGATGCTATTCATAAAATACCTACACAAATTCCGGTAT 4	2/0/ IAAGIIACLIGOCAIICAIIIGACIGCAIICAIIACHAGUIIACHAGUIIACHAGUIIIACHAGUIIACHAGUIIACHAGUIIACHAGUIIACHAGUIIACHAGUIIACHAGUIIACHAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	1 AATCATCTCCTTAGGAGATTCATAATTAAAATCCATTCTATAACATTACGTAATTGTCT 300	1 1 1	121 TAAATACTGTCTTTCAAATTCTTCACGAGCTTTACGTAATGGTACAGAAATAACTTTAGC 180

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Best Local
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Publication No. US20030044422A1
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CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/269,944
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 EQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Ehrlichia Ruminantium Polypeptides, Antigens, Polynucleotides,
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: UF-299XC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barbet, APPLICANT: Whitmi
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LOCATION: (1)..(984)
LOCATION: (1)..(984)
OTHER INFORMATION: Corresponds to SEQ ID NO:52, nucleotides 632..1615
OTHER INFORMATION: Hypothetical glycerol 3-phosphate dehydrogenase
OTHER INFORMATION: Product = "19hworf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 984
TYPE: DNA
TYPE: DNA
ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium)
FEATURE:
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                                                                    ACACAACAATTACGCACCATATGTACACAAATACAACACACAAACAGCATATGTGTAAAAAT
                                    ACACAACAATTACGCACCATATGTACACAAATACAACAGCAGAACAGCATATGTGTAAAAAT
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Mwangi, Duncan M.
McGuire, Travis C.
Mahan, Suman M.
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Simbi, Bigboy H
Ganta, Roman R.
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100.0%; Pred. ...
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APPLICANT: Ganta, Roman R.
APPLICANT: Moreland, Annie L.
APPLICANT: Moreland, Annie L.
APPLICANT: Moreland, Annie L.
APPLICANT: Mosaire, Travis C.
APPLICANT: Mosaire, Travis C.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Enrichia Ruminantium Polypeptides, Antigens, Polynucleotides,
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: UF-299XC1
CURRENT APPLICATION NUMBER: US/10/081,051
CURRENT APPLICATION NUMBER: US/60/269,944
PRIOR APPLICATION NUMBER: US 60/269,944
PRIOR APPLICATION NUMBER: US 60/269,944
PRIOR APPLICATION NUMBER: 2001-02-20
NUMBER OF SEQ ID NOS: 117
SOPTWARE: Patentin version 3.1
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barbet, Anthony F.
APPLICANT: Whitmire, William
APPLICANT: Kamper, Sondra M.
APPLICANT: Simbi, Bigboy H.
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                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Barbet, A.
APPLICANT: Whitmire
APPLICANT: Kamper,
APPLICANT: Simbi, B
APPLICANT: Genta, R,
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Best Local Similarity
APPLICANT: Kamper, Sondra M.
APPLICANT: Simbi, Bigboy H.
APPLICANT: Ganta, Roman R.
APPLICANT: Moreland, Annie L.
APPLICANT: Moreland, Annie L.
APPLICANT: Mosaire, Duncan M.
APPLICANT: McGuire, Travis C.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Ehrlichia Ruminantium Polypeptides, Antigens, Polynucleotides, and TITLE OF INVENTION: Methods of Use
FILE REFERENCE: UF-299XC1
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OTHER INFORMATION: Complement to SEQ ID NO:52,
OTHER INFORMATION: Hypothetical cell division;
OTHER INFORMATION: Product = "19hworf41"
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Whitmire, William M.
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Pred. No. 2.5e-85;
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CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/269,944
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin version 3.1
SEQ ID NO 53
SEQ ID NO 53
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LOCATION: (1)..(371)
COTHER INFORMATION: Complement to SEQ ID NO:52, nucleotides <1..371
OTHER INFORMATION: Hypothetical integrase/recombinase
OTHER INFORMATION: Product = "19hworfli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 371
TYPE: DNA
ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium)
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                                                                                                                                                                                                                                                                                                     121 AGTGACCTTGCATTGGTAACTGCTTCAACTCCACATTGATATCTAGAAGCAAACCATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATACCTCTTCTTCCTTCCATCCATATTTTCCAATTATTTACAATATCATAGAGTTCT
                                                                         GAATACCTCTTCTTGTTCCATCCATATTTTCCAATTATTTACAATATCATAGAGTTCT
                                                                                                                                                  TTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAACTGTATTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAACTGTATTCAAA
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TTATTCGACAT 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 371; pred. No.
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Sequence 5. Application US/10010160
Fublication No. US20030103999A1
GENERAL INFORMATION:
APPLICANT: Rosey, Everett L.
APPLICANT: Strugnell, Richard A.
APPLICANT: Strugnell, Richard A.
APPLICANT: King, Kendall W.
APPLICANT: King, Kendall W.
APPLICANT: King, Kendall W.
APPLICANT: ROSE, ROSETT T,
APPLICANT: ROSE, ROSETT T,
APPLICANT: ROSE, ROSETT T,
APPLICANT: ROSE, ROSETT T,
APPLICANT: NUMENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR
TITLE OF INVENTION: TREATING INFECTION BY LAWSONIA SPP.
FILE REFERENCE: DAVIIIO.001AUS
CURRENT APPLICATION NUMBER: US/10/010,160
CURRENT APPLICATION NUMBER: AU PR1381
PRIOR APPLICATION NUMBER: NU PR1381
PRIOR APPLICATION NUMBER: US 60/249,596
PRIOR APPLICATION UNUMBER: US 60/249,596
PRIOR APPLICATION UNUMBER: US 60/249,596
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1371
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US-10-010-160-5
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Best Local Similarity 52.1%;
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3379 ATTAATCATACTTCTCAAATTACGTATAACAGGGGAGTTACCGACTATTTCATAATCCTC 3438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2482 ACACAATCCAAGAATTTTCAATTTACGGTGTAATGCTGAACGTTCCAATCAACTAATTC 2541
                                                                                                                                                                                                                                                     3259 CATAGATATAAATGGAGTATCATACCCCTTGGATTTTTTATGTATTAGCCTAGCAACTAC 331
                                                                                                                                                                                                                                                                                                                                                               3199 ACTTTCCTCACTACCAAATATATTAACCAAGTAATTATTAGCTGGTAGCATAGATGAGTA 3256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1119 CCCTGAATAAAGAATAACCATTCGTTCTACAAAATTAAGTAATTCTCTTACATTCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                      699 TTTÄTGTGCCAACTCAÄAACGACCTGCACGAGAAGCATCGGCACCAGTAÄÄGGCC-----
                                                                                                                                                                                                 AACAGCTATAAATGGTTTTTGATATCGTGAGCTTCCTTTGTGCAATGCTTGTGCAGCTAA 526
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                                                                                       CTCTTTACCTGTACCATTCTCTCTGTAAGTAGTACCCAAGCATCTGTTGGAGCGACCTG 466
                                                                                                                                         TTCCTTTCCAACACCTGGCGAACCAGTAATGAGTATACGACTCGATGTAGTAGCTGCTTT 3378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATTTGCTTTGCTCTATAATTCCAATATGAGGAGGTACTCTATGAGACACATATATTATT 3198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: ED/1/208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       Matches 1233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3673778
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
  1715588 ÁTTCCTCTÁÁAACCÁCTCCTÁTTACCÁAÁÁTCTATACTAATCAAATTTTTCTAAÁÁAAACÁ 1715529
                                                                                                                                                                           3796 TAGATTTCTGATATCAACTTCATCAACAACTAATA 3833
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                                          259 AACTTATCAAGGTCTCTTACATAAGAAACAACTGTATTCAAAGAATACCTCTTCTCTTGT 318
                                                                                                                                                                                                                    199 ACATGCACAAGATTATTTAATGTAACAGAACACCCTGTACTCTTATGCAAGAACTCTATA 258
                                                                                                                                                                                                                                                                                                            139 ACTGCTTCAACTCCACATTGATATCTAGAAGCAAACCATTTTCTCAAATCTCCAATTTTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 -- GAAGCCAAATATCAAGAAAAACAAGATCTGGAGACTCTACATCAACACCACTTAAGTCC 112
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45.4%; Pred. No. 3.9e-22;
ative 0; Mismatches 1447; Indels 37; Gap
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US-10-282-122A-16370
                                                                         PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 16370
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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LENGTH: 1017
TYPE: DNA
ORGANISM: Clostridium botulinum
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                                                                                                                                                                                                                                                           FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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FILING DATE: 2000-11-27
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FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
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FILING DATE: 2000-09-06
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APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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FILING DATE: 2000-12-22
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Zyskind, Judith
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Malone, Cheryl
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Carr, Grant
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US-10-282-122A-16370

US-10-282-122A-17353 ; Sequence 17353, Application US/10282122A ; Publication No. US20040029129A1

GENERAL INFORMATION:

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; ORGANISM: Clostridium difficile
US-10-282-122A-17353
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 17353
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APPLICANT: Zamuc
APPLICANT: Malo
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                            874 ACAACAATTACGCACCATATGTACACAAATACAACACAAACAGCATATGTGTAAAAAATAC 933
                                                                                                                                                                                                                                                                                  198 TACTGATATAGAAAAACTATAAAAGATTGTAAGGTA---ATAGTTTTAGCAGTTCCATC 254
                                                                                                                                                                                                                                                                                                                                                           814 CAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTAC 873
                                                                                                                                                                                                                                                                                                                                                                                                                             138 AACTAAAGAAAATACAGACTATTTACCAGGAGTATTATTTCCAAATAATATAACTATAAG 197
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309 AGTTATTGTTAATGTAGCTAAAGGTCTTGAAAAAGGGACTGGGCTTAGATTATCACAAGT 368
                                                             934 TCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAAT 993
                                                                                                                                       255 ACAGGCTGTAAGAAGTACTTGCCAAAAAAATA-----AAACCATTTATAAAAGAAGGACA 308
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Forsyth, R.
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Malone, Cheryl
Haselbeck, Robert
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51.6%; Pred. No. 2.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35500, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                        FILE REFERENCE: ELITRA 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                    PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                   PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Xu, H.
ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILING DATE: 2000-09-09
                              FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
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PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 35500
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                           1355 TCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTT 1414
                                                                                                                                                                                                                                                                                                                                                                             1175 ATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATC 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 CÁCCATCAAAATAAACGTTATTTAAAAGATGTCGTTTTAGATAGTAGAATTAAAGCAACT
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468; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 AATGGACATACTGTTTTAATGTGGGGAAAAAATGAAGATAGTGTGAAAGAATTAAATGAT
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                                                                                                                                                                                                                                                               AGTGATATTAAAGAAGCCGCGAATTTTACTGATATATTTAATGGCTCTACCAACTAAA
                                                                                         ATAAGCCGATTAGGTGAAAAATTAGGTGCT----GATCCAATGACATTTTTAGGTCTT
                                                                                                                                                ATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCA 1354
                                                                                                                                                                                                       GCAGGCATGGGCTATGGTGATAATGCTAAAGCTGCTTTAATGACACGAGGTTTAGCTGAA
                                                                                                                                                                                                                                                                                                                         GTCGGTGTTGAACTAGGAGGAGCATTAAAAAATATAATTGCAGTTGCAAGTGGTATTGTA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACTGATTCAAGATTTATTATGAATGATTATTTACGTGTATACACTAATAATGATTTA
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US-09-815-242-8974
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                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-815-242-8974
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8974
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                            Matches 505; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus aureus FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(999)
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                                                                                                                                                                                                                                                                                                                      y Match 3.5%; Score 168.6; DB 9; Length 999; Local Similarity 51.4%; Pred. No. 2.6e-17; hes 505; Conservative 0; Mismatches 454; Indels 24
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                                                                                                                                                               695 CATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACT 754
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                                                     755 TACCGAAAAATTTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACC 814
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                                                                                                          67 AÄTGGACATGATGTTTTGATGTGGGGGTAAAAÄTCAAGATGCTGTTGATGAATTÄÄÄTACA 126
                                                                                                                                                                                                                    7 AAAATTACCGTTTTTGGTATGGGAAGTTTTTGGGACAGCCCTTGCCAATGTTCTTGCAGAA 66
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TGTCATACAAATAAAAGTATTTAAAATACGCGAAATTAGATGTTAACATCATCGCTACT 186
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Trawick, John D.
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US-10-282-122A-15395
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                                                                                                                                                                                                                                                                                                                                       Sequence 15395, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1586 GATAAAGCCATATCAAACATATT 1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1346 ATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAAT 1405
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                    Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR FILING DATE: 2001-02-09
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 15395
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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TYPE: DNA
ORGANISM: Clostridium acetobutylicum
   1128 AAACAATAAGTAATGATGTTCTAAAAATAATAATACCATCAAGATATTATAGGTGTACAGA 1187
                                                                                                                                                           1068 АТСІТССІТСТАСТАГАСТАСТІССІССІСАТААТАЛАСААСТІССІСААТСАТІСАТАС 1127
                                                                                                                                                                                                                                                                                                                                                    311 TTGCAAAAGGCATGGAAGAAGAGACCAAGAAGAGGCTGTCTGAAGTAGTTAAAGAAGAAGAAC 370
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
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                            APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
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APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
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FILING DATE: 2000-05-26
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Malone, Chery
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Yamamoto, Robert
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 34158
LENGTH: 999
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  1526 AATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTA 1585
                                                                                            1466 CTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTT 1525
                                                                                                                                                                                                             1406 ATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAAATACATTAATAGATCACAAC 1465
                                                                                                                                                                                                                                                                                                                  1346 ATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAAT 1405
                                                                                                                                                                                                                                                                                                                                                                                                                       1286 АТGААТGАААТТААААСАСТАТАТАТАССААААААТСАТТСААТАGATCTTCATACATTA 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1166 CAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGT 1225
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                                                     832 AATATGGTTGTAGAAGGTATTTATACAACTAAATCAGTTTATCATTTAGCTAAAGAAAAA 891
                                                                                                                                                          772 TTCACATTAGGÁTATAÁACTTGGÁCÁÁGGTGAÁTCAÁTGGÁTCAÁGCÁTTÁTCTGÁAÁTG 831
                                                                                                                                                                                                                                                               712 CTAGGTTTAGGTGGTATCGGTGACTTAATCGTTACTTGCATATCAACACATTCTCGAAAT
                                                                                                                                                                                                                                                                                                                                                                     658 TTAGCGGAAATTAGTAGA-----TTAGGTGAAAAGTTAGGTGCCGATCCTATGACATTT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 GATGACTTGATTGGTGTTGAACTTGGTGGTGCATTGAAAAATATCATCGCAGTAGCAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               935 CCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAATA 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AAAGCAATGCGAGAAGTTGCTACTCAAATTAATGATAAGC-----TGACCTCTAAAAAG 297
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Pred. No. 8.5e-17;
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PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 252
LENGTH: 7814
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-10-221-714A-252/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 5013.1005

CURRENT APPLICATION NUMBER: US/10/221,714A

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: PCT/EB01/02955

PRIOR FILING DATE: 2001-03-15

PRIOR FILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-03-15

PRIOR PRIOR DATE: 2000-03-15

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.3%;
Local Similarity 44.0%;
es 945; Conservative 0
                                                                                                                                                                                          5401 AAAÁAÁATÁÁTTÁAATÁÁATÁÁATÁÁATAÁATAAACATÁTAAACÁAACCAÁAACAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5581 АЛТААСАААСАСТААЛААСТТАСААЛААТАЛАЛААТАЛАЛАЛААСАТААТАЛАЛАЛАТАЛА 5522
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5341 АТААСАСАСАСБААТАААТАААТАААСАССТСАААССТАААССТАААТСТТАТААААТААА 5282
                                                                                                                                                                                                                                                                                       5461 TTĊTĊCATTATACAATATATCCATAAAACAAAACTACATTTATACCCCCTTACATTTATAC 5402
                                                                                                                                                                                                                                                                                                                                                                                   5641 TACCTATTCTCATATATAAATAAAAACTAAATAATATATACACATAAACATAAAATATAA 5582
                                                                                                                                            671 GCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCAT 730
                                                                                                                                                                                                                                        611 TTGATATAAATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACA 670
                                                                                                                                                                                                                                                                                                                                491 ATTTATTATACTACTCATCATATTTAGCATAATATCACATCTGACATGATTAACAATAGT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 ААТАGTCTTTAGCAAGAACTACAAATATAATGAGACACTTAACTTATTAATATATTTCAA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         952 AAAGAATGCGTAAAAGATTTAAT 974
                                              AGAAATATTACACATATAAACACTTACCGAAAAATTTTAAAATATTTACCCACATATCAT 790
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                              1808 CCTATCTCAATTAACCAATTGTTATCAGATTATAAATAAGTCAAATTAAACTTTTACTTA 1867
                                                                                                                     4264 CAACACTATTCATAATAACAAAAATACAAAATCAACATAAATATCCATCAACGAATAAAT 4205
                                                                                                                                                                      1748 ATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACAAATTCCTATCT 1807
                                                                                                                                                                                                                    1688 ATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATTAC 1747
                                                                                                                                                                                                                                                                                                                1568 CATGAGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTT 1627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1508 TCATTAGCAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTA 1567
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RESULT 15
US-10-282-122A-21770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                            FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang,
                                                                                                                                                                                                                            TLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4084 ТАСБАРАСБАРАЛЕСТАРАЛАСТАРАЛАТСРАТАСТАСТАТТСТСАТАРАЛЕСТССТАРАЛА 4025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1981 ACCTATTTACTACGTAATATTACATAGATGTCCTGACAT-AATAAATTCTATCATCCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2457 CATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTA 2506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCTATTATAACAAATTCAAGAATTATATATACTTCACCAACACATAGTTATCAAATTC
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Zyskind, Judith
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Malone, Cheryl
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Forsyth, R.
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PRIOR FILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21770
LENGTH: 1065
TYPE: DNA
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PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 49.0
les 504; Conservative
                                             1062 CAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCAT 1121
                                                                                                                                                                                                                                                                                                                                                                                                                            1002 AAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTG 1061
                                                                                                                                                                                                                                                                                                                                                                                 427 GAA--GAAAAAAGACAGGCAATTGTTGTATTATCTGGTCCTAGCCATGCTGAGGAAGTGG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 AAAGGACTAGAACAAGATACGCATAAACGAATCTCAGAAGTTTTGGCTGAAGAAATTCCA 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 TCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAA 763
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     TAGGATTCGGAGATGATGCAAAAGCAGCAATCATGACTCGAGGATTGGCAGAAATCAGCC 724
                                                                                                                                           TACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAA 1241
                                                                                                                                                                                        TACAAAAACTGTTCATGAATGATTATTTCAGGATTTATACAAATAATGATGTGATTGGCG 604
                                                                                                                                                                                                                                      ТGАТАGАЛАСААТААGТААТGАТGТТСТААЛААТААТАТАССАТСААGАТАТТАТАGGTG 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACGCACCATATGTACACAAATACAACACAACAGCATATGTGTAAAAATACTCCAATAT 941
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                                                                                             TAGAAACTGGTGCAGCACTGAAAAATATCATTGCAATTGGTGCCGGCGCTATCCATGGAT 664
                                                                                                                                                                                                                                                                                   CAGTACATGATATCACAACTATTACAGCTGCAAGTATTGATCAAAAAAGCAGCAGCCTATG 544
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49.0%; Pred. No. 3.9e-15;
ative 0; Mismatches 515; Indels 10
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US-10-311-455-1369/c
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Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1369
LENGTH: 5641
                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1027;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.3%; Score 155; DB 14; Length 5641; Best Local Similarity 43.9%; Pred. No. 7.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: cytosine methylation FILE REFERENCE: 5013.1014 CURRENT APPLICATION NUMBER: US/10/311,455 CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR EILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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APPLICANT: PIEPE
APPLICANT: BERLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
4829 ACGÁTATAATTATTTCAACTACTTCAÁAACTAÁAAAAACTCAATÁTTAÁAÁÁAATAÁTÁTÁ 4770
                                                                                                                                                                                                4946 ATTAAATAAAAACATAAAAATAAACAAAATCAACATTTTCTTAAAAATTAAAAATCTTA 4887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1362 TTGGAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAG 1421
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                                           296 TCAAAGAATACCTCTTCTCTTGTTCCATCCATATTTTCCAATTATTTACAATATCATAGA 355
                                                                                                                                                                                                                                                   236 TACTCTTATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAACTGTAT 295
                                                                                                                                                                                                                                                                                                                                                  176 ATTTTCTCAAATCTCCAATTTTAACATGCACAAGATTATTTAATGTAACAGAACACCCTG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 959 TTACTCAAACAATCTATAATGTTTTGTATAATGGAGAAGATATCAAAAAAGCAGCAAAAG 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         839 TGTTAGGACAGGGACATAAGCTGGAAGAAGTTCTAGAAAACATGGGAATGGTCGTTGAGG 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             779 TGGGGGACTTGATCGTTACTTGTACAAGTGTTCATTCTCGCAATTGGCGTGCCGGTAACT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               725 GTCTTGGTGTCĠĊGÀTGGGT-----GCCAÀTĊCTĊTGÀĊÀTTTÀTCĠĠTTTGAGTGĠTG 778
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                     3706 AAACATACTAAAAATTAAAATACTATAATATACCTT----TTTTTCCTTCGAAAACCTAA 3651
                                                                                                                       3766 ATATAATTAATTTCGAAAAACTAATTCGAACAATATTTTATATCTTATCAAACACATTTA 3707
                                                                1432 AGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTAC 1491
                                                                                                                                                                          1372 AATATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAA 1431
                                                                                                                                                                                                                                                                         1312 AGCAAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCATCATGTCTTTGGAGATCT 1371
                                                                                                                                                                                                                                                                                                                       3876 AACAAATTAAATTTAAATACACTATATATTAACCGATAAATTCTACATAAATACACTCTAT 3817
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2326 САРАРАСТСАЛАСТСТАТТАТАКАРАЛТТСАЛСАРАТТАТАТАТАСТТСАССРАСАСАТАС 2385
                                                                                                                                                                                                                                                                                                                                                                                                                           2870 АТТТАТТТАААЛААСТАСАСАТАТАЛАААЛАСТСGАСАЛАСТТТАЛАСАЛАДТАЛАТАСЛА 2811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1848 TCAAATTAAACTTTTACTTATTATAAAATAATATGTTTGCACACTTTTTCACTACATCA 1907
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                                                                                                            AACAAACTTCTCAACAAAAACAAAAAAACTCCAAAACAATTAAATAACATATTCAAAAT
                                                                                                                                                              AAATAATTATACATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTT 2505
                                                                                                                                                                                                                                                                                                                 CTCABABABATATABABACACCATTABACCATACCAACATAAAATACAAATACTABBA 2931
                                                                                                                                                                                                             TTATCAAATTCTATAATACATCATATCCTTTTTAAAAAGATGACTTCACAATTCATACAT 2445
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US-08-781-986A-513/c
US-08-781-986A-513/c
; Sequence 513, Application US/08781986A
; Publication No. US20030054436A1
; Publication No. US20030054436A1
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
TITLE OF SECUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
COMPUTER: HP Vectra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Benson, Bob
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
  1382 TGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAAT 1441
                                                                                                                                                                                                             1142 GATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTA 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1082 АТАСТАСТІССТССТСАТААТААДААСТІССТСАДТСАТІСАТАСАЛАСЛАГАДСТАДІ 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1022 ATTTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGT 1081
                                                                                                                                                                                                                                                                                                               1202 AAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAAAATTTAGGTAATAATGCT 1261
                                                                                                                                                                                                                                                                                                                                                                      612
                                                                                                                                                           492 AAAGCTGCATTAATGACTCGTGGCTTAGCCGGAAATTAGTAGA-----TTAGGTGAAAAAG 439
                                                                                                                                                                                                                                                                  552
                                                       438 TTAGGTGCCGATCCTATGACATTTCTAGGTTTAGGTGGTATCGGTGACTTAATCGTTACT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.2%;
Similarity 53.6%;
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                                                                                                         CATTCAATAGATCTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACA 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                      GATTATTTGCGTGTGTACACGAATGATGACTTGATTGGTGTTGAACTTGGTGGTGCATTG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAATATCATCGCAGTAGCAAGTGGTATCGTAGCTGGAATTGGCTACGGTGATAATGCA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maryland
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US-10-329-624-513/c
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                                                                                                               US-10-329-624-513
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Query Match 3.2%; Score 154.2; DB 12; Lengtl Best Local Similarity 53.6%; Pred. No. 4.9e-15; Matches 346; Conservative 0; Mismatches 293; Indels
                                                                                                                                                                                                                                                                        TELEPHONE: (240) 314
TELEPAX: (301) 309-8
INFORMATION FOR SEQ ID NO: 513
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 513:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 27-Dec-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Charles Kunsch
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                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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STREET: 9410 Key West Avenue
CITY: Rockville
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                                                                                                                                                                                                                                              LENGTH: 918 base pairs
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                                                       Length 918;
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                                                                                                                              CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: CCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR PELINGTON NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2128
LENGTH: 15548
  ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-2128
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Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C APPLICANT: BERLIN, Kurt
                                                          FEATURE:
                                                                               ORGANISM: Artificial Sequence
                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1562 TTATTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATC 1621
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AGGTAATAATGCTGTTGCTACTGTTATAACTAAAGGCATGAATGA	1189 TGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAAAATTT 1248 12577 ATAAAATATATATAATATATATATATATAAAATATATACATAAAATATATATATATATATATATA 12518	ATĀTATĀCGAAATĀTĀTĀTĀTĀTĀTĀTĀTĀTĀTĀTĀTĀTĀĀTĀTĀ	1137 GTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTACAGAT 1188	1077 GTAGTATAGTACTIGCTGGTGATAATAAAGAACTIGGTGAATCATTGATAGAAACAATAA 1136	1017 ATCCAATTITATACTCTCTGGTCCAAGITTTGCTAAAGAAATTGCAGAACATCTTCCTT 1076 1	957 GTATCGAAATTACATCACTCAAATTTCCCAGTGAAATAGCAGAAGAAATTTTACAATATA 1016	12818	CACAATACAACACAACAGCATATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAG 956	837 CTGACAACAATACATGTATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTA 896	777 TACCCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTAT 836	TATATATATACATATATATATAAAATATATATACAATATACAATATAAAATACA 12997	776	657 GATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTAT 716	597 TTTTGACTGGTTTCTTGATÄRAATTAGGTÄAAAAAATGAAAATCAGTÄTTTÄGGTGCAG 656 13176 ATATATAAAATATATATATATATATATATATAAAATATAT	TATATATATA-AAATATATATATATATATATATATAAAATATATATATATA	TGATTAACAATAGTAACACATTTCTTAACACTAGATAATATACAATAATATATAT	477 TIPATATATITOARATTTATTATACTACTCATATATTAGCATARTATCACATCTGACA 536	417 ATAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAGACACTTTAACTTA 476	ATATAAAATATATACGTATAAAATATATAAAATATATATA	416	CARAGAATACCTCTTCTTCTTCCATCCATCTTTTTCCAATTATTTACAATATCATAGAG 356	13534 ACACATACGTATAAAATATATATATAAAACACATACGTATAAAATATATACGTATATATA	l; Conservative 0; Mismatches 1185; Indels 27; Gaps 9;	3.2%; Score 153; DB 14; Length 15548;
OY 2327 AAAACTCAAAGTTCTATTATAACAAATTCAAGAATTATATATA	Db 11505 AATAAAATATATAAAATAAAATAAAATTATATTCCATTACATTATT	2267 атаатаадааладатодттатдаттатасааттасаалатттоссаасттсаасаас	OY 2207 TAAACATAGGAACCAATAGTATATACTACTACTAAGTAAG		11681	DD 11741 AATATAAAAATAAAATATAAAATAAAATATAAAATATAAAA	2027 TCTRICATCCTTGACATATTTCAAAACATAAAATATGATAAACTGTTTTTTTATGCCCATT	Qy 1967 TAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATAAAT 2026	Db 11861 AATAAAATAAAATATAAAATATAAAAATATAAAAATAAAA	11921	1847 GTCABATTABACTTTTACTTATTTATABAAATAATATGTTTGCACACCTTTTTCACTACATC	Qy. 1787 TATATAAACAAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATTATAAATAA	CATATAAAATAAAATATAAAAATATATATAACATATAAAAATAAAAATATATATA	12097	Db 12157 CTATAAAAATAACATATATATATATAAAAAATAACATATAACATAGAAAA 12098 Oy 1667 ATAGAATACAACGTTCACCACATATAATAAAAAAGAGCAGTCAAATACCCATCGTTAACATCCA 1726	1607 TTATCTTAGTCTATCATCCTTTGATAATTTCAACACAATGATAAATAA		Db 12277 ATATATATATAACATATATATATATATATATATATATAT				L.		

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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Apoptosis
FILE REFERENCE: 5013.1006
CURRENT APPLICATION NUMBER: US/10/240,452
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03969
PRIOR APPLICATION NUMBER: PCT/EP01/03969
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
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LENGTH: 6314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Local Similarity 44.9%;
les 1058; Conservative
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                                                                          170 CAAACCATTTTCTCAAATCTCCAATTTTAACATGCACAAGATTATTTAATGTAACAGAAC 229
                                   590 ATATAATTTTTGACTGGTTTCTTGATATAAATTAAGGTAAAAATGAAAATCAGTATTTTA 649
                                                                                                                                                                                                                                                                    410 CTAATTAATAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAGACACT 469
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TTTATACTCTTCCTTACGCTATAAAT---AAATACCACAAAAAACAAATCTTAATTATAT 4866
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                                                                                                              Score 148.8; DB 14; Length 6314; Pred. No. 7.5e-14; O; Mismatches 1267; Indels 29; Gaps
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                    3845 ААААААААААСТААСААСGААААААААТТССАААААСБАТАААААА --АААСААТААСАА 3788
                                                        1664 AATATAGAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACAT 1723
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                                                                                               АТАЛАТАЛАСЛАТАЛСАТАЛЛАЛАЛАЛАЛАСССАЛЛАЛАТТАЛЛАЛАЛАСЛАЛЛАЛАТАТА
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                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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Forsyth, R.
                                                            Trawick, John
Carr, Grant
                                                                                                                         Wall, Daniel
                                                                                                                                                      Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                  Haselbeck, Robert
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 6338
LENGTH: 1020
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITEA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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                                                         1107 AACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCATC 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               749 AACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATAT 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GCCGAAAATGGACACGAGGTCTGTATTTGGGGGAAATAAACCAGAGCAAATCGATGAAATA 123
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CAGACÓCTÓTGTATGTÓCAAGAGTTGTTTATGAATGATTACTTTAGAATTTATACGAATG 541
                                                                                                                   ATGCAGAAGAAGTCGCTGTTCATGACATTACAACCATTACAGCAGCAAGCGAAAATTTAG 481
                                                                                                                                                                            TTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAG 1106
                                                                                                                                                                                                                                         GCGGAAGAGTTCCAGCAGA--ÀAAACGGCAAGGGATTGTGGTTTTATCTGGTCCAAGCC 421
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                                                                                                                                                                                                                                                                                                  GTGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTT 1046
                                                                                                                                                                                                                                                                                                                                                            ATTATTCATGCAAGTAAAGGGCTCGAACAAGGTACACATAAGCGGATTTCAGAAGTGATA 363
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RESULT 22
US-09-815-242-6755
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                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: 09/09/815/242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                  PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 6755
LENGTH: 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6755, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                ORGANISM: Enterococcus faecalis
                                                              TYPE: DNA
      FEATURE:
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; LOCATION: (1)...(1023)
US-09-815-242-6755
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Best Local Similarity 49.1%; Pred. No. 4.3e-14;
Matches 483; Conservative 0; Mismatches 491; Indels
1587 ATAAAGCCATATCAAACATATTAT 1610
                                                                                                                         1527 ATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAG 1586
                                                                                                                                                                                                                                         1467 ТАРА ССТТСТТСРА А ССРАСТАСТ СТАРА В ССРСТСТВ ТЕТЕТ ТО СЕВТЕТ В 1526
                                                                                                                                                                                                                                                                                                                                                                      1407 TGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAAATACATTAATAGATCACAACC 1466
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                                                           896 AAGTCGAAATGCCAATCACAGAAACAATCTACAATGTCTTGTACAATGACGAAGATGTAC 955
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                                                                                                                                                                                    836 GCATGATTGTGGAAGGTGTTTCAACAACTAAAGCAGCCTATGAATTGGCACAACAACTAG
                                                                                                                                                                                                                                                                                                       776 GÉCGTGCGÉGTAATTTÁTTÁGGÁÁÁÁÁGÉCCATÁÁGTTÁGÁTGAÁGTCTTÁGAAAAAAACATGG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASCSEQ for Windows Version 4.0
SEQ ID NO 3869
LENGTH: 1026
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.1%; Score 147.2; DB 9; Length 1026; Best Local Similarity 49.1%; Pred. No. 6.6e-14; Matches 480; Conservative 0; Mismatches 488; Indels 10;
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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APPLICATION NUMBER: 60/206,848
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           993
                                                                                                                                                                                                               304 CATGCAAGTAAAGGGCTCGAACAAGGTACACATAAGCGGATTTCAGAAGTGATAGCGGAA
                                                                                                                                                                  184 ACTGATTTAGCCACTGCTTTAGTAGATGTGGATGCGGTACTGTTTGTGGTACCAACTAAA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                               755 TACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACC 814
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  TAGCAGAAGAAATTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGCTA 1052
                                                                                                            CTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCCAGTGAAA 992
                                                                                                                                                                                                                                                                                                                         AGCAATATAGACGAAGTATTATCTGACAACAATAC--ATGTATTATCTTAACTATTCCTA 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr, Grant
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                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 836
LENGTH: 6132
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Publication No. US20030143606A1
GENERAL INFORMATION:
  Query Match
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
                                                              FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1533 AACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAG 1592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       776 CGGGTAATTTÄTTÄĞGÄÄÄÄĞGCCATÄÄGTTÄGÄTGAÄGTCTTÄGAAAÄCÄTGGGCATGA 835
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Score 147.2;
DB 14;
Length 6132;
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1300 AACACTATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCATCATG 1359	1240 AAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAACTAAAGGCATGAATGA	1181 GTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATA-ATCGCTGG 1239	1121 TTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGT 1180	1061 GCAGAACATCTTCCTTGTAGTAGTAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCA 1120	1001 GAAAITTTACAATATAAATCCAATTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATT 1060	941 TTAAITTGIAGTAAAGGTAICGAAATTACATCACTCAAAITTCCCAGTGAAATAGCAGAA 1000	881 TTACGCACCATATGTACACAAATACAACAACAACAGCATATGTGTAAAAATACTCCAATA 940	821 ATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACAACAA 880	761 AAAAATTTAAAATATTTACCCACATATCATCTACCAGACATATATGGAACCAGCAAT 820 	701 ATATCAGTTAACCTTATGGGGACGTGATCATAGAAATATTACACATATAAACACTTACCGA 760	641 AGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACAGTGGT 700	581 ATAAATAATATATATATTTTGACTGGTTTCTTGATATAAATTAAGTAAAAAAATGAAAAATC 640	521 AATATCACATCTGACATGATTAACAATAGTAACACATTTCTTAACACTAGATAATATACA 580	461 TGAGACACTTAACTTATTAATATATTTCAAATTTATTATACTAC	401 TAGTACTATCTAATTAATAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAA 460	341 TTACAATATCATAGAGTTCTTTATTCGACATACATATTAAAATCAATC	281 AAGAAACAACTGTATTCAAAGAATACCTCTTCTTGTTCCATCATCATATTTTCCAATTAT 340	Best Local Similarity 44.2%; Pred. No. 1.3e-13; Matches 1069; Conservative 0; Mismatches 1318; Indels 31; Gaps 10;
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D d	S B &	S B :	S B 7	δ <u>β</u> ;	δ β ;	Q & &	S B &	D 4	S B &	S & S	? B &	S & &	S B &	? B \$	S B &	S B 7	S B :	6 B
2958 TATATAAAATATCCAAAAATAATAATTACAAATTTTAAATATACTAAATATCACTAAATT 2899	10 ACLICACIONES CARROL CARROL CONTROL	77 TTATTTTTCCATTAAAAAAGGAATACTACAACATATACTACAACTTATATAAAATCTCAAA		97 AATTTATACACAAATACTTATTATTACTACATTAACTAAATAACCAAAAAA	57 CCAAAAATATATATTTAATATATATOCAAAAAAAACTAAAACATATTATTCATACAAA 36 CTGCAACAATATATAGAAGAAGATACAATATA		ARABARATA I BRANTI BRU PARRACKUU BAII BRU BRUGARATA KUBARATA KARIBARATA KARIBARA KUBARATA KARIBARATA KARIBARA K	TO THE CARCINATION AS A TRANSPORT OF A CONTRACTOR OF THE CANTENDA A CANTENDA CONTRACTOR OF THE CANTENDA CANTENDA CONTRACTOR OF THE CANTENDA CONTRACTOR OF TH	1930 TATAMATANG CAMATITANG TITANG TATAMATANAN TATAMATA	70 CIAGCIANI INIA INGRAMI INCLAICI NICIA INCOMINI INCOMINI MENERALI NICIA NICIA NICIA NICIA NICIA NICI	10 IAMAKI CANCIANGIA ISIANGIA IKA IKAKAMAKI IIANGIA IMPOLITANGIA IMPOL	77 TACAAAATAAAAAAATATTTACAAACCACATATCTAATAA	1590 CHANCHIALIA LULASUCLIA CALCALIVALINA LURCACACACIGA AMAZERANG 100 A	97 AATTCTTAAATTTAACACCAAAAAACACCAAAAAAAAAA	57 AAACCATAAAACTCTTAAAAAAAAAAACGTAATCTTCATAATTTCTAATTTTCTAATATCAATA	3917 CTACCTTATATCACATAAATAAATTAAATTAAATCAATC	77 TCTTCAACAAATAATAACTAAAACAATTAAATAACCATATAACAAAATACTCTAATAA	4037 TITAATTTTTAATAAAATTATCAAAAAATCTTAAACATTCAATAAAAAA

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913 ACAGCATATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAAATTACATC 972

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US-10-398-221-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.1%;
Best Local Similarity 49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10398221 Publication No. US20040018514A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Listeria innocua, genome and applications FILE REFERENCE: 344 702 - US CURRENT APPLICATION NUMBER: US/10/398,221 CURRENT FILING DATE: 2003-03-27 CURRENT PRIOR APPLICATION NUMBER: PCT/FR 01/03 061 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061 PRIOR FILING DATE: 2001-10-04 PRIOR APPLICATION NUMBER: FR 00/12 697
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APPLICANT: GLASER, Philippe
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(end)
OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
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52178 TGTCGTGATTGCTATTCCAACAAATGCAATGCGTGTGGTTTGTAAGCAGCTAAATGAAGC 5223
                                                                                                                                                                                                                                                        52061 AATTGTGAATGAAATTAACGAATCGCACACGAATAGTCACTATTTGCCAGATATTATTTT 52120
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                                                             853 TATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAA 912
                                                                                                                                                                                       793 ACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATG 852
                                                                                                                                                                                                                                                                                                                  733 АААТАТТАСАСАТАТАААСАСТТАССВАААААТТТААААТАТТТАСССАСАТАТСАТСТ 792
                                                                                                                                                                                                                                                                                                                                                                                                                                               673 AATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGGACGTGATCATAG 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 GATATAAATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGC 672
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Pred. No. 8.9e-13;
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                           ; ORGANISM: Listeria innocua
US-10-398-221-2058
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                                                                                                                                        SEQ ID NO 2058
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Publication No. US20040018514A1
GENERAL INFORMATION:
                                                                                                                                                                                                 APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
NUMBER: OF SEQ ID NOS: 4025
CONTRADER: DESCRIPTION 3 0
                                                                                               TYPE: DNA
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                               2064537 TCGÁGÁÁTÁAÁ 2064527
                                                                                                                                               2064597 GTTGGGCGAAAAACTAGATATTGATATGCCAATTACCGAATCGATTTACGCGATTTTAT 2064538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2064774 ---ATCCACĂAĂCCTTTTACGGGCTĂACTGGTATTGGTGĂCTTĀATCGTTĀCTTGTĀCAĀ 2064718
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                                                                                    1569 ATGAGAATATA 1579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 AATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAG 732
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0; Mismatches 473; Indels 14; Gaps
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CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/PP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR PLING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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PRIOR APPLICATION NUMBER: DE 10032529.7
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PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
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LENGTH: 11745
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Publication No. US20030148326A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.1%;
Best Local Similarity 43.5%;
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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associate
TITLE OF INVENTION: With DNA TRanscription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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LOCATION: (9105)
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   5609 TTAAATACTAAAAACACACCAAAAAAACAAAAACCAAAATCCCTCCCTCAATAACTTACATT 5550
                                                                                                                   5789 AAAATTTATAAAAATTÄÄTÄÄTTAAAAAATTTTAAATATCAATAATTÄAÄÄÄÄCTTACAÄ 5730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            748 AAACACTTACCGAAAAATTTAAAATATTTACCCACATATCATCTACCAGACAACATATA 807
                                                                                                                                                                        688 GTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATTACACATAT 747
                                                                                                                                                                                                                                                                                        628 AAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACT 687
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TGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTAT 867

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4717 ATCAATAACTCTATTTTAACCGTATCAAAATACTCATTACACATCTACCTAAAAATATTA 4658
1646 GATAAATAAACGGTCAAAAATATAGAATACAACGTTCACCACATATATAAAAAGCAGTCA 1705
                                                                                                                                 4539 АЛЛАЛАЛАЛАСАЛАТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАС----САЛЛАЛСАЛАДАЛАСТАДАТСАС 4485
                                                                                                                                                                                                                                                                                                       4599 TTTAAAATACATCACAATAAAATAATATTTAAAACCTTAAAATTAACTCGAATCACCTA 4540
                                                                                                                                                                                                                                                                                                                                                                                          1766 АСТТАЛАЛТТТССТАССТАЛТТАТАТАЛАСАЛАТТССТАТСТССТАТСТСАЛТТАЛССАЛ 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4657 АЛТАЛССАСТАТАТАТАТАЛАЛСТАА - АЛСТТАЛАЛАЛАЛАЛАТААЛСТАЛАЛАЛССАТТ 4600
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3824 AATTCTT 3818
                                       2545 AGTTCGT 2551
                                                                          2305 CAAAATTTCCAACTTCAACAACAAAACTCAAAGTTCTATTATAACAAATTCAAGAATTAT 2364
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                                                                                                                                                     ATGACTTCACAATTCATACATAAATAAATTATACATGCAATGTTTATTCAGAAACATTACA 2484
                                                                                                             CAATCCAAGAATTTTCAATTTACGGTGTAATGCTGAACGTTCCATTCCAACAAATTCAGC 2544
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RESULT 28
US-10-311-455-986/c
Sequence 986, Application US/10311455
Publication No. US20030143608A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
ITTLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
ITTLE OF INVENTION: Cytosine methylation
ITLE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 986
LENGTH: 7597
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Best Local &
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                                                                                                                                                                                                         2132 АТТССТВСААСААТАТВААВАВАВАТАСААТАСАСБТСАААТАААТТАААСАААТТТСТАА 219:
                                                                                                                                                                                                                                                                                           2072 TTTTTATGCCCATTAGTTCTTAATAAATTGCTAATTACCCAAAAAGGTTAAAATACAC 2131
                                                                                                                                                                                                                                                                                                                                                                                 2013 CTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATA-AAATATGATAAAACTGT 2071
                                      2251 CTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTATATTTATACAATTACAAAAT 2310
                                                                                                                          672 ATAAATÄAATAAATAAACÄCÄTÄÄATÄÄATAÄÄTAAATAÄATÄÄÄTÄCGTÄÄATÄÄÄTAÄ 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             792 ААТАААТААААААТАААТАААТАААТАААТАААТАССТАААТАААТАААССДААТААТААА 733
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47.4%; Pred. No. 4.3e-13;
ative 0; Mismatches 613; Indels 4;
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US-10-312-841-2/c
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CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 3673778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10312841 Publication No. US20030186277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.0%; Score 141.6; DB 14; Length 3673778; Best Local Similarity 43.8%; Pred. No. 1.2e-11; Matches 1001; Conservative 0; Mismatches 1269; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH
FILE REFERENCE: E01/1208/WO
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NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (379615)
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                                                                                                                            2091974 ACTACTAAACCACTAA-----TACTAAATTAATTTAACACATTAATAAACTACAAAAATCA 2091920
                                                                                                                                                                                                            2092094 АДАСААТАРАРАТАААТАААТАААТСАТСТАРАТТАРАРАДАТАРАРАТАРАРАСТАТСТСАР 2092035
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                                                                                                                                                                                                                                                     674 ATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGA 733
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                                                                                                                                                                 734 АЛГАТТАСАСАТАТАЛАСАСТТАССБАЛАЛАТТТАЛАЛАТАТТТАСССАСАТАТСАТСТА 793
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854 ATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAAATACAACAAA 913
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2091080 AAAAACATAACCCCTTTAAAAAAACAACTAACAATAACTCAAATTTATAAACATTAAATT 2091021
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1929 TACATAAAATAACTAACTAAAAAAAGAACCAATACATATATTAAATTAC-TAAAACACCCTATT 1987
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                                                  2647 ACTTAAAA 2654
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US-10-398-221-3618
US-10-398-221-3618
Sequence 3618, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederik
APPLICANT: KUNST, Frederik
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
FURRENT APPLICATION NUMBER: US/10/398,221
CURRENT APPLICATION NUMBER: DS/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SEQ ID NO 3618
SEQ ID NO 3618
LENGTH: 2791
TYPE: DNA
ORGANISM: Listeria monocytogenes 4b
FEATURE:
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; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
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1554 GTTGGGCGÁÁÁÁÁÁCTAGÁTATTGÁTATGCCÁÁTTACCGAATCGATTTÁCGCGATTTTÁT 1613
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                                                       CATTAGCAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTAC 1568
                                                                                                                     AAGTATTAGAAAAAATGGGCATGGTCGTTGAAGGTGTTCGAACAGCTAAAGCAGTACATG 1553
                                                                                                                                                                                                                                          GTGTGCATTCACGTAATTGGCGTGCTGGTAATATGCTAGGTAAAGGCGAGAATTTAGATG 1493
                                                                                                                                                                                                                                                                                                                                                               CTAATCCGCAAACATTTTACGGATTGACAGGTATTGGTGACTTAATCGTTACTTGTACTA 1433
                                                                                                                                                                                                                                                                                                                                                                                                                          TAGATCTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAA 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            СТБТТАТААСТАЛАББСАТБААТБАЛАТТАЛААСАСТАТАТАТАБСЛАЛАЛЛАТСАТТСЛА 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGCTGTAAAGATTTATCAGCTGCTGAAATTGTTCAAGATCGTTTCATCAATAATAATT 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTAATGACTCGCGGGATGGCAGAAATCACTCGTCTCGGTGTTGC-----TGTTGGCT 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAAAATAATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACA 1208
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Pred. No. 1.5e-12;
0; Mismatches 477; Indels 14; Gaps
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APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
ITILE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT EDILICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 800;
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ORGANISM: Artificial Sequence
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5526 AAACTTAATATAAAATATATAAAAAATATATATAAAATAAAATAAACATATATAAAAC 5467
                                                       1220 GCATGTGGAATAATCGCTGGAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAACT 1279
                                                                                                                     5586 TAACATATATAAAATATTAACATATATATAAACATAAATTTATAAACATAAATATATATA
                                                                                                                                                                         1160 TACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAATT 1219
                                                                                                                                                                                                                                       5646 TATAAAATATAAACATATATAAAATATAAACATATAAATAAATATAAATATATAAAATAT
                                                                                                                                                                                                                                                                                              1100 AATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAATA 1159
                                                                                                                                                                                                                                                                                                                                                            5706 ТАСАДАТАТАТАТАЛАСАЛАТАТАТАТАЛАЛАТАЛАЛАТАЛАЛАТАЛАДАСАТАТАТАЛАДА. 5647
                                                                                                                                                                                                                                                                                                                                                                                                                      1040 CCAAGITITGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGTGAT 1099
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45.8%;
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Pred. No. 2.7e-12;
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1460 CACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAA 1519
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2359 AATTATATATACTTCACCAACACATAGTTATCAAATTCTATAATACATCATATCCTTTTT 2418
                                                                                           4476 TAAATATAAACATAAATAAATAATTACATTATATTTAAACATAAATATAAATAAATATAA 4417
                                                                                                                                                                                                                                                                                      4536 ATATATACATATATAACAACATATATATAATCAAATACATTATACGTATAAACGTATA 4477
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                                                                                                                                                                                 2299 CAATTACAAATTTCCAACTTCAACAACAAAACTCAAAGTTCTATTATAACAAATTCAAG 2358
                                                                                                                                                                                                                                                                                                                                                                       2239 AGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTATATTTATA 2298
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US-10-311-455-227/c
Sequence 227, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 227
LENGTH: 18154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.9%; Score 137; DB 14; Length 18154; Best Local Similarity 44.0%; Pred. No. 8.4e-12;
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: ECT/EPO1/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
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                                               14825 AACCTAACÁCÁAACÁTAACCTACAACTATAATAAAÁAÁTTTAAACACAACTTTATTÁAAAAA 14766
                                                                                                                                                                                                                                                                                                                                                                                                                                                 14945 TAĀTATCAĀAAĀĀATAĀAATCCATĀTTCAĀAĀCĀATAĀTAĀTĀATĀATĀAAAACATATA 14886
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                                                                                                                                                                                                                                                                                               660 CATTIGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGG 719
                                                                                                                                                                                                                                                                                                                                                                                              600 TGACTGGTTTCTTGATATAAATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGAT 659
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840 ACAACAATACATGTATTATCTTAACTATTCCTACACAACAATTACGCACCATATGTACAC 899
                                                                                               780 CCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTG 839
                                                                                                                                                                                              720 GACGTGATCATAGAAATATTACACATATAAACACTTACCGAAAAAATTTAAAATATTTAC 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 1285; Indels
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1734 ANGTAACATATTACATAACATAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAA 1793 13761 TCCCACCTCAAAAAACAACACAAAATATTATAACAAATTTTACCAAAACTTAATATATA 13702 1794 ACAAATTCCTATCTCCTATCTCCAATTAACAATTATACAAACAAATTTTACCAAATTATACAAAT 1853 13701 AACAATTAATTCTAATCTTATTATAAAATAATTTTAAAAAA	TRATTRAACTTTCAAACACACATATAAAAAATTTAAATTTAACTTTAATTTAATTTAATTAAAAATTAAAAAA
RESULT 33 US-09-815-242-6968 ; Sequence 6968, Application US/09815242 ; Patent No. US20020061569A1 ; PATENT NEFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Zyskind, Judith W. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Yanamoto, Robert T. APPLICANT: Yanamoto, Robert T. APPLICANT: Xu, H. Howard ; TITLE OF INVENTION: Identification of Essential Genes in	Db 1359 TAACTTATATTACTTCTAAAACAATTTTAAAATAATAATA

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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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PRIOR APPLICATION N
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LOCATION: (1)
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Local Similarity 50.4%;
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                                               1154 ATAATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATT 1213
                                                                                                                                               1097 GATAATAAAGAACTTG----GTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAA 1153
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535 GTTTATATAAATTCGGATATGACTGGCGTTCAACTTGGTGGAGCAATTAAAAATGTGATC 594
                                                                                                475 AATAACGAGCAATTCGCACGGGÄÄTTTCAGTCTCGTATTCATTGTÄGTAAAGGTTTCCGA 534
                                                                                                                                                                                              415 GECCCAACTTTTGCAAAAGAATTAGCGCAAGGTCTACCATCAGCTATTACGCTTGCTGCC
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Pred. No. 2.9e-12;
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RESULT 34
US-10-882-122A-22052
Sequence 22052, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22052
LENGTH: 1008
                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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Trawick, John
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Zyskind, Judith
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Forsyth, R.
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TYPE: DNA ORGANISM: Haemophilus influenzae

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   1334 CTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAA 1393
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889 GCACAAAGACAAGGTGTGGAAATGCCGATTACAGAACAAATTTA 932
                                                                                                                                                                                                                                                                                                                                                            709 ACCAATACATTTATGGGAATGTCTGGATTGGGCGÁTTTAGTGCTAACTTGCACCGATAAT 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 GATCTTCATTTAGAAAGTAATCTTGCACAAGCAAT---GGAATATTCTCAAGATATTTTA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 GCACAAATGCAGACAGAACGACAAAATTATCGTTTTTTGCCGGATGTCATCTTTCCTGAG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620 ATTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCA 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 АСАСАТАТАДАСАСТТАССGАЛАДАЛТТТАЛАЛТТТАСССАСАТАТСТАССАGAC 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680 ATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATT 739
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                                                      GCAAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTA 1557
                                                                                                                ATGGAAAATATCGGGCAAGTCGTAGAAGGTTTTTATAATACAAAAGAAGCCTATTTGCTT 888
                                                                                                                                                                              ATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTA 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACTCGAGGTATTGCAGAAATTACCCGCTTAGGTATCTC-----GCTCGGTGCAAAT 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTTATATAAATTCGGATATGACTGGCGTTCAACTTGGTGGAGCAATTAAAAATGTGATC 594
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                                                                                                                                                                                                                                        CAATCGCGCAATCGACGTTTTGGATTAATGCTAGGTAAAGGATTAGATGCCCAAATGGCT 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAATTGGTGCGGGTATTTCAGACGGTATGGGGATTTGGCGCAAATGCTCGCACAGCACTG 654
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RESULT 35 US-10-329-960-1

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CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN VETSION 3.1
SEC ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10329960 Publication No. US20030099277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fra
TITLE OF INVENTION: Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PB186P1
FEATURE: misc feature NAME/KEY: misc feature LOCATION: (45732)...(45732) OTHER INFORMATION: n equals a,
                                                                      LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals
                                                                                     NAME/KEY: misc_feature
LOCATION: (45593)..(45593)
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LOCATION: (44975)...(44975)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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LOCATION: (36636)..(36
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LOCATION: (36551)..(36
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LOCATION: (36543)...(36543)
OTHER_INFORMATION: n equals
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LOCATION: (29298)..(29
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LOCATION: (10150)..(10
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OTHER INFORMATION: n equals
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LOCATION: (44905)..(44
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LOCATION: (44416)..(44416)
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NAME/KEY: misc feature
LOCATION: (120038)...(120038)
OTHER_INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a,
                                                                                                                       NAME/KEY: misc feature
LOCATION: (119324)..(119924)
OTHER INFORMATION: n equals a,
                                                FEATURE:
                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (119750)..(119750)
OTHER_INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals
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LOCATION: (51805)..(51805)
OTHER_INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (51334)..(51334)

OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a, t,
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LOCATION: (105121)..(105121)
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LOCATION: (102696)..(102696)
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OTHER INFORMATION: n equals a,
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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LOCATION: (47036)..(47
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JOCATION: (80024)..(80
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THER INFORMATION: n equals a,
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LOCATION: (51786)..(51
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OTHER INFORMATION: n equals
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LOCATION: (51602)..(51
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ACATION: (117136)..(1
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INFORMATION: n equals
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INFORMATION: n equals a,
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Best Local Sim
Matches 476;
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NAME/KEY: misc_feature
LOCATION: (152530)..(152530)
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals a,
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LOCATION: (140398)..(140398)
OTHER_INFORMATION: n equals a,
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a,
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LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a,
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,
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LOCATION: (142750)..(142750)
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OTHER INFORMATION: n equals a,
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LOCATION: (122336)..(1)
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LOCATION: (122167)..(122167)
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LOCATION: (147197)..(147197)
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                                                         635291 GCACAAATGCAGACAGAACGACAAAATTATCGTTTTTTGCCGGATGTCATCTTTCCTGAG 635350
                                                                                                                                   635231 ATTACCTTTTCTCGCAATGGTTCTCCCACTCACTTATGGGGGCACAATCCCCGCCCATATC 635290
                                                                                                                                                                                                          635171 ATAACTTCGCAAACACCAATCACTGTGCTAGGTGCGGGATCTTATGGAACTGCGCTGGCA 635230
800 AACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATC 859
                                                                                           740 ACACATATAAACACTTACCGAAAAAATTTAAAATATTTACCCACATATCATCTACCAGAC 799
                                                                                                                                                                     680 ATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATT 739
                                                                                                                                                                                                                                          620 ATTAGGTAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACAGCAATAGCA 679
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PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOPTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
LENGTH: 1830121
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10329670 Publication No. US20040018503A1 GENERAL INFORMATION:
                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-12-24
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                         FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,670
CURRENT FILING DATE: 2002-12-24
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome,
TITLE OF INVENTION: Thereof, and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635702 GTTTATATAAATTCGGATATGACTGGCGTTCAACTTGGTGGAGCAATTAAAAATGTGATC 635761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1274 ATAACTAAAGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGAT 1333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCCAAGTTTTGCTAAAGAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGT 1096
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals
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LOCATION: (47036)...(47036)
OTHER INFORMATION: n equals
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LOCATION: (9921)...(9921)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a,
                                                                                              NAME/KEY: misc feature
LOCATION: (51786)...(51786)
OTHER INFORMATION: n equals
                                                                                                                                                                                                     OTHER INFORMATION: n equals
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LOCATION: (51602)..(51
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LOCATION: (45732)..(45
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LOCATION: (45593) ...(45593)
OTHER INFORMATION: n equals
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LOCATION: (44975)...(44975)
OTHER_INFORMATION: n equals
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LOCATION: (44416)...(44416)
OTHER INFORMATION: n equals
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LOCATION: (40808)..(40
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LOCATION: (36636)..(36636)
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LOCATION: (36551)..(36
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NAME/KEY: misc_feature
LOCATION: (36543)...(36543)
OTHER INFORMATION: n equals
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LOCATION: (29298)..(29298)
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (4747)..(474
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LOCATION: (44905)..(44
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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FEATURE:
NAME/KEY: misc feature
*COMMICON: (65309)..(65309)
NAME/KEY: misc_feature
LOCATION: (139910)..(139910)
OTHER_INFORMATION: n equals a,
                                                        NAME/KEY: misc_feature
LOCATION: (131360)..(131360)
OTHER_INFORMATION: n equals a,
                                                                                                              NAME/KEY: misc feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a,
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LOCATION: (55369)..(55369)
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a,
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LOCATION: (65313)..(65
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JOCATION: (122167)..(122167)
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JOCATION: (120038)..(120038)
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OCATION: (119750)..(119750)
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DTHER INFORMATION: n equals a,
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LOCATION: (100091)..(100091)
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TION: (107248)..(1
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INFORMATION: n equals
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Best Local Similarity 50.4%;
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LOCATION: (152500)..(152500)
OTHER_INFORMATION: n equals a,
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NAME/KEY: misc feature
NAME/KEY: misc feature
147197)..(147197)
170N: n equals
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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LOCATION: (145058)..(145058)
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LOCATION: (142750)..(142750)
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LOCATION: (140398)..(140398)
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                                                                                                                                                          635522 TTACTACAAACCGTAGTTGAAGAACAACTCGGAACGCAATATCCACTAGCTGTACTTTCT
                                                                                                                                                                                                                                                                                                                                    635408 ATCGTGGTGCCAAGCCATGCTTTCGGTGAAATTCTTATAAAAAAT-----CAAACCGCAC 635461
                                                                                                                                                                                                                                                                                                                                                                                                                            635351 GATCTTCATTTAGAAAGTAATCTTGCACAAGCAAT---GGAATATTCTCAAGATATTTTA 635407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      635231 ATTACCTTTTCTCGCAATGGTTCTCCCACTCACTTATGGGGGCACAATCCCGCCCATATC 635290
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                                                                                                                                                                                                                                                 635462 TTAAAAGCCCATCACCGATTAATTTGGGCAACAAAAGGTTTGGAACGTAACACAGGGCGT 635521
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1097 GATAATAAAGAACTTG----GTGAATCATTGATAGAAACAATAAGTAATGATGATGTTCTAAAA 1153
                                                                                                                                                                                                    977 AAATTTTCCCAGTGAAATAGCAGAAGAAATTTTTACAATATAATCCAATTTTTATACTCTCT 1036
                                                                                                                                                                                                                                                                                       920 ATGTGTAAAAATACTCCAATATTAATTTGTAGTAAAGGTATCGAA---ATTACATCACTC 976
                                                                                                                                                                                                                                                                                                                                                                                 860 TTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACAGCAT 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    800 AACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTATTATC 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 ACACATATAAACACTTACCGAAAAAATTTAAAATATTTACCCACATATCATCTACCAGAC 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   680 ATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAATATT 739
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                                                                  GGCCCAACTTTTGCAAAAGAATTAGCGCAAGGTCTACCATCAGCTATTACGCTTGCTGCC 635641
                                                                                                             GGTCCAAGTTTTGCTAAAGAAATTGCAGAACATCTTCCTTGTAGTATAGTACTTGCTGGT 1096
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435 Qy	375 QY 10999 Db	315 Db	10; Db	Db	Q VQ	Qy	dd Qy	gg Qy	em by Determ Db	β	Qy	Qy Ob	1513 Qy 636055 Db	1453 Qy 635995 Db	1393 Qy 635935 Db	1333 Qy 635875 Db	1273 Qy 635821 pb	1213 QY 635761 Db	635701 Db
1451 TTAATAGATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCA 1510	1391 GAACATTCACGCANTATGGCTTTTGGACTAGAANTAGGAAAAGGTAGAAATTATTATCA 1450 		6 AAC	ATCTCAACTACTACACTTTCAATTTTTAAAAATACTAATTAAATTTACATAATA	AATTGCATGTGGAATAATCGCTGGAAAAAATTTAGGTAATAATGCTGTTGCTACTGTTAT	1156 AATATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGC 1215	1096 TGATAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAAT 1155	1036 TGGTCCAAGITTTGCTAAAGAATTGCAGAACATCTTCCTTGTAGTAATAATACTTGCTGG 1095	976 CAANTTTCCCAGTGAAATAGCAGAAATTTTAAAATATAATCCAATTTTATACTCTC 1035	GCATATGIGIAAAAATACICCAATATTAATTIGIAGIAAAGGIACICGAAATTACACCACCATAATATATATAATAAAAAAAAATTAAATAAATAAT	TATCTTAACTATTCCTACACAACAATTACGCACCATATGTACACAAATACAACACAAACA	796 AGACAACATATATGCAACCAGCAATATAGACGAAGTATTATCTGACAACAATACATGTAT 855	736 TATTACACATATAAACACTTACCGAAAAAATTTAAAATATTTACCCACATATCATCTACC 795	676 AGCAATTGCACTGTCAGCACATGGTATATCAGTTAACTTATGGGGACGTGATCATAGAAA 735	616 ATAANTTAGGTAAAAAATGAAAATCAGTATTTTAGGTGCAGGATCATTTGGCACGGAT 675	556 ATTICITAACACTAGATAATATACAATAATATATATATATTITGACTGGTTICTTGAT 615	496 TTATACTACTCATCATATTTAGCATÄATATCACATCTGACATGATTAACAATAGTAACAC 555	436 TCTTTAGCAAGAACTACAATATAATGAGACACTTAACTTATTAATATATTTCAAATTTA 495 	10998 ATAAAAATAAAAAAAACTCAACTAAATTTTTTTAAACATTTTATTTTTT

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2520 AACGTTCCATTCCAACAAATTCAGCAGTTCGTGATACATTACCTCCAAAACGAGATAACT 2579
                                                                                                                                                                                                                                             2460 GCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTACGGTGTAATGCTG
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                                                                                                                                                                 TAAAATAATATTTCAÄÄTAÄAAÄACTTÄAATÄÄÄÄÄTCTATÄTCTACAAAACACÄÄÄAAA
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PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1999
LENGTH: 17594
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                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1999
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                                                                                                                                                                   Query Match
Best Local Similarity 45.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
7810 ATRAATAAAAAAAATTAATAAATTTAAAAATATATATTAATAAACTTACTAACAAAT 7751
                                                                                             8371 CAACAAC 8365
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                                            405 ACTATCTAATTAATAAAAAAATCCTCAATAGTCTTTAGCAAGAACTACAAATATAATGAG 464
                                                                                                                                         2760 ATTGTCTTAAGTTACCTGGCCATTCATATGACTGCATTGCTATTA--AAGCTTCATCACT 2817
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                                                                                                                                                                                       2.9%; Score 136; DB 14; Length 1:
45.0%; Pred. No. 1.2e-11;
ative 0; Mismatches 1190; Indels
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TTGCATATCTATTTACAATTTACATGAGAATATATCACTAGATAAAGCCATATCAAA 1602	ACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTA-GAACTACCAAT 1542 		GAGATCTAATATTAACATGTACAACAGAACATTCACGCAATATGGCT-TITGGACTAGAA 1423	TATATATAGCAAAAAATCATTCAATAGATCTTCATACATTAATTGGTCCATCATGTCTTG 1364	ATTTAGGTAATAATGCTGTTGCTACTGTTATAACTAAAGGCATGAATGA	AGATTGGAGCTGCATTAAAGAACATAATTGCAATTGCATGTGGAATAATCGCTGGAAAAA 1244	TAGAAACAATAAGTAATGATGTTCTAAAAATAATATACCATCAAGATATTATAGGTGTAC 1184	AACATCTTCCTTGTAGTATAGTACTTGCTGGTGATAATAAAGAACTTGGTGAATCATTGA 1124	TTTTACAATATAATCCAATTTTTATACTCTCTGGTCCAAGTTTTGCTAAAGAAATTGCAG 1064	TTTGTAGTAAAGGTATCGAAATTACATCACTCAAATTTCCCAGTGAAATAGCAGAAGAAA 1004	GCACCATATGTACACAAATACAACACAAACAGCATATGTGTAAAAATACTCCAATATTAA 944	ACGAAGTATTATCTGACAACAATACATGTATTATCTTAACTATTCCTACACAACAATTAC 884	ATTTAAAATATTTACCCACATATCATCTACCAGACAACATATATGCAACCAGCAATATAG 824	CAGITAACITATGGGGACGIGATCATAGAAATATACACATATAAACACTTACGGAAAAA 764	TTTTAGGTGCAGGATCATTTGGCACAGCAATAGCAATTGCACTGTCAGCACATGGTATAT 704	ATAATATATATTTTTGACTGGTTTCTTGATATAATTAGGTAAAAATGAAAATCAGTA 644	TCACATCTGACATGATTAACAATAGTAACACATTTCTTAACACTAGATAATATACAATAA 584	ACACTTAACTATATATATATTTCAAATTTATATACTACTA

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                                    2498 TTCAATTTACGGTGTAATGCTGAACGTTCCATTCCAACAAATTCAGCAGTTC 2549
                                                                                                            2438 TCATACATAAATAATTATACATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATT
                                                                                                                                                6029 ACTATATTCAAACATTATACTTTATCCTATTTAATACTCACAAAAATCCTATAAAACAAA 5970
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RESULT 39
US-10-311-455-1460/c
US-10-311-455-1460/c
; Sequence 1460, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:

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US-10-311-455-1460
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TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION OF Section 101460
LENGTH: 6831
TYPE: NAME OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF
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APPLICANT: PIEPENBROCK, Christian
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                   5987 ATTTTAAACAAAAAACTTTATAAAAAATCACTCTCGTTACTATAAAACAACTACGAAAA
                                                                                                                                                                                                                                      6164 TCTCTTTAAATAAAAATAAACTTAACAAAACTAATAAAAACA---ACATATAATAATAA
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                                                                                                                                                                      891 TATGTACACAAATACAACACAAACAGCATATGTGTAAAAAATACTCCAATATTAATTTGTA 950
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   4848 AAACTAAACAATAAATCTAAATTCAAATTTAAATCTAACTCCAAAACTTATAATCTTTCC 4789
                                                        1998 ТАТТАСАТАGATGTCCTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATAAA 2057
                                                                                                                                   4908 CTCAABAAAAATAAAATTTAAAAAAATCACGAAACATACTTAACTTAAAAATCATA 4849
                                                                                                                                                                                                   4968 ÄATATAATAAATATAATATCÄAACACTTATTTTTÄAÄÄTAÄÄACACTTTTTACGCÄÄTT 4909
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	3071 AATAATCTGAGTAATCTTAATTGCGTATCGTATCGTAAATCTGTTACTTCATCTATAAAT 3130	3016 CACATCTATACTAACAGGAATCTTACTATTTTCCCTATATATTTTTCCCTCCTGT 3070	2956 ACAAAACCTACCAGCTTTTACTTCACTTTCAATATCTTTGGAAGAAGAACAACAATAATTCT 3015 3898 TATAATATTACCATCACTTAACAATCATTTAATAATTTTTACTAC	2896 ATATTCTACTAAAGACGGTACTCTAATTGGAAGGACATTTAATCTATAATATAAATCCTC 2955	2836 ACCTATTTTTTACAGATGCTATTCATAAAATACCTACACAATTCCGGTATATCTGTACA 2895	2718 TAGGAGATTTCATAAATCATTCATTAACATTACGTAATTGTCTTAAGTTACC 2775	2658 CATTAATAGGCGAATTAGATACTATATCTACTGGTAAATCTTTTGCTGTAATCATCTCTC 2717	2598 TITGAAATTCTTCACGAGCTTTACGTAATGGTACAGAAATAACTTTAGCACTTAAAACAT 2657 4258 ATATAAAATACAATCATTTTATTCTCAAAACTCAAAAAAA	2538 ATTCAGCAGTTCGTGATACATTACCTCCAAAACGAGATAACTGAGTTTTTAAATACTGTC 2597 4318 AATAAATTATTAAAAATACTTAAAAAAAAAAATATTTATTA	2478 CATTACACAATCCAAGAATTTCAATTTACGGTGTAATGCTGAACGTTCCATTCCAACAA 2537	2418 TAAAAAGATGACTTCACAATTCATACATAAATAATTATACATGCAATGTTTATTCAGAAA 2477	2358 GAATTATATATATCTTCACCAACACATAGTTATCAAATTCTATAATACATCATATCCTTTT 2417	2298 ACAATTACAAAATTTCCAACTTCAACAACAAAACTCAAAGTTCTATTATAACAAATTCAA 2357	2238 AAGTAAGATATCCCTACAGCATGTATCAAAITAATAAAGAAAAATCGTTATGTATATTTAT 2297 4615 AAAAACCACCTAACTCTATTTTATTACAAAITAAAATAATACACATCAAATTCACTCCCAAC 4556	2178 AAACAAATTTCTAATATAACCACCTACTCTAAACATAGGAACCAATAGTATATCATACCT 2237	2118 AGGTTAAAATACACATTCCTGCAACAATATGAAGAAGAAACACATACACGTCAAATAAAT	4788 ACATTTACCTACTATCTCAAATTCATAAAATAATTAAAAAA
QY 4210 AAAACTCACTTGAAGCTTTATAGATATTCAATAATTCACGCCAAGCAGCATAAGAATCAT 4269	OY 4150 TAAATTATTTATATTATATCCTTCCCTGGAACACCCATGTTATAGTTTTCCATACTA 4209	4090 AAAAACACTTAATAAAAACTTATCAACTTTGTAAACCTAATACTAACTA	4030 TAGTTACTATTATTATCAAGCATAGGTTCCTATATATCCAAAAAGAAAAT	3970 ААСААССААГАТАТТАРАТТСАТТАТТТТТАСТТАТАРАТТТАДАСАТАТТАТАРАРАТ	3910 GCAAACACAATGTACTCCTTTAAAGTACACCTCATAATACTACCACCACACCACACTTATGATC	QY 3790 TITTATTAGATTTCTGATATCAACTATCATCAACAACTAATACTTCAGAAATATACAA 3849	3730 GATCGCGGATAAACCATCAACTGCTAATTTAGTGACATAATTATCATCACTTAATATATCT 	3670 AGRICCTUTTACCATATATCCACATCATGCATCATCATCATCATCATCATCATCATCATCATCATCATC	3610 ACAGGGAATAAGGATACCTTTTTTTTTTTTTTTTTTTTT	3551 GCCCCATATIGCAGAGACTITACAGAGTGGCAATATTACCATGCCCACT-AATCATAAT	3491 GCICICITIACAACIITAACTICITCITCITIAGAAAGGCTITICIAGIIAAICAICAA 3358 TTAATTTTAAACAAATCTAATAAATCTATTTTTCCATAAATATATACCTAAACA	3431 TRATCCTCRAATGCTGATTTCAACTCATCATTTTCTCTACGTAATCTACCAGACTCTATA	3371 3478	3311 GCAACTACTTCCTTTCCAACACCTGGGGAACCAGTAATGAGTATACGACTCGATGTAGTA	3251 3598	3191 ATATTATTACTTCCTCACTACCAATATATTAACCAAGTAATTATTAGCTGGTAGCATA	3/18 AAAACTAAAATATTATTCACAATAAATATTCGATTAAAFTCCTATTTTCTAAAAAAAAAA

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CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRICA APPLICATION NUMBER: PCT/EP01/07537
PRICR FILING DATE: 2001-07-02
PRICR APPLICATION NUMBER: DE 10032529.7
PRICR FILING DATE: 2000-06-30
PRICR FILING DATE: 2000-06-30
PRICR APPLICATION NUMBER: DE 10043826.1
PRICR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
LENGTH: 11691
TYPE: DNA
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US-10-311-455-2214/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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2.9%; Score 135.4; DB 14; Length 11691;
Local Similarity 44.6%; Pred. No. 1.3e-11;
hes 972; Conservative 0; Mismatches 1176; Indels 31;
                                                             3727 CTATAAATCACACACACACCTAACCATTACTTAAATCCAAAAATACTATACTTAAATAT 3668
                                                                                                                                                                                                                                                                        3787 CÁAAATAAAAATAAAAACCGAAÁCAAATTTCCÁTCCCTTTTAAATÁAAAATAACÁTAÁCÁ 3728
                                                                                                                                                                                                                                                                                                                                                                         3847 AACAACACAATACTTAACGCATAATCAATACCCAATTATTAACATTCAAAAAATTTATT
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        482 ATATTTCAAATTTATTACTACTCATCATATTTAGCATAATATC---ACATCTGACATG 538
                                                                                                                                                                                                                422 АЛЛАТССТСАЛТАСТСТТТАССАЛСАЛСТАСЛАТАТАТЛАТСЯСАСТТАЛСТТАТТАЛТ 481
                                                                                                                                                                                                                                                                                                                       302 AATACCTCTTCTCTTGTTCCATCCATATTTTCCAATTATTTACAATATCATAGAGTTCTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 TATGCAAGAACTCTATAAACTTATCAAGGTCTCTTACATAAGAAACAACTGTATTCAAAG 301
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                                                                                   2601 ÁCÁTTTTTATTAATTTCÁÁAÁCAAACATÁTCTÁAAATTCAÁAAÁCTCÁCGATÁCGTAÁTT 2542
                                                                                                                                                                                       1497 AACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTT 1556
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1768 ACAATTATATTTAATACTA 1750
                                                                                              1828 AMACTCAACTTTAATTAAAAATTTAATCAACATTCTTACTTACTTACTAATTAACTATTTTATA 1769
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                                            2392 AATTCTATAATACATCATA 2410
                                                                                                                                        2332 ТСАЛАСТТСТАГТАТААСАААТТСААСААТТАТАТАТАСТТСАССААСАСАТАСТТАТСА 2391
                                                                                                                                                                                                                                                                                                                                                                                                                                           2067 АЛТАЛАЛАТТТАЛЛАЛАЛАЛАЛАЛАЛАТАЛАСЯТТАЛАСТТАТСЛАТАТТСАССАЛТАТТ 2008
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Search completed: April 6, 2004, 02:08:18 Tob time : 1628 secs

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Result
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                        157.2
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DEFINITION
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122.8
121.8
121.8
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Xenopodinae; Silurana.

1 (bases 1 to 1626)

1 (bases 1 to 1626)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: Ggapbs-r@mail.nih.gov

Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation can be
Clone distribution: MGC clone distribution information can be
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Silurana tropicalis
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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IMAGE: 6995950 5', mRNA Bequence.
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_Emb6 Silurana tropicalis cDNA clone
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CG749499 P043-4-AA

CG747831 P041-3-BA

CG747831 P041-3-BA

CG746828 P044-1-CA

CG749728 P044-1-CA

CG749728 P044-2-CA

CG749728 P044-2-CA

CG74915 P035-3-EA

CG75114 P045-3-EA

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97 CH261-36A
89 CH261-62N
15 Tetraodon
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                         1933 ТАРАНТАНСТАНТАНАНАБАКСАНТАСАТАТАТТАНАГТИСТАНДАСИССТАТТТАСТА 1992
                                                                                   1873 AAAATAATATGTTTGCACACTTTTTCACTACATCATGTATAATGAACATAATTTTACA 1932
                                                                                                                                                                                                     1753 AAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACAAATTCCTATCTCCTAT 1812
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                                                                                                                 http://image.llnl.gov
Plate: LLAM14680 row
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                                                                                                                                            ATTTCAACACAATGATAAATAAACGGTCAAAAATATAGAATACAACGTTCACCACATATA 1692
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/lab_host="PH10B (phage resistant)"
/clone lib="NICHD XGC_Emb6"
/note="Vector: pCWV-SPORT6.1; Site_1: Not1; Site_2: EcoRV;
/note="Ucctionally Primer: Oligo dT. Average insert size_2.1 kb. Consetructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                 An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                         1 (bases 1 to 1896)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
                                                                                                                                                                                                                                                                                                                                                                           CG753083.1 GI:37977199
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence CG753083
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Similarity 42.9%; Pred. No. 1.6e-13;
60; Conservative 0; Mismatches 1000; Indels 11;
   AAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATT 1555
                                                                                                                                                                                                       ТАААААААААТАТАТАТАТААТАТААТААТАТТИВАДАТАДАДАТАДТАДАДАДАДАДАД 1229
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/db xref="taxon:54126"
/db xref="taxon:54126"
/clone lib*"ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC
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/mol_type="genomic DNA"
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Local Similarity 37.5%;
1392 AACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGGTAGAAATATAAAATACAT 1451
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                                                                                                   1332 ATCTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAG 1391
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                                                              972 CACTCAAATTTCCCAGTGAAATAGCAGAAGAAATTTTACAATATAATCCAATTTTTATAC 1031
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CG748014
CG748014.1 GI:37968940
GSS
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

1 (bases 1 to 1531)
1 (bases 1 to 1531)
2 rinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R. J.
Buntjer, J., van der Meulen, M. and Sommer, R. J.
An integrated physical and genetic map of the nematode Pristionchus
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/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."
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/mol_type="genomic DNA"
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966 TIACATCACTCAAATTTCCCAGTGAAATAGCAGAAGAATTTTACAATATAATCCAATTT 1025	786 ATCATCTACCAGACAACATATATGCAACCAGCAATATATAGACGAAGTATTATCTGACAACA 845	Y Match Local Similarity 35.8%; Pred. No. 1.4e-12; Local Similarity 35.8%; Pred. No. 1.4e-12; hes 577; Conservative 0; Mismatches 1030; Indels 3; Gaps 1; 726 ATCATAGAAATATTACACATATAAACACTTACCGAAAAATTTAAAATATTTACCCACAT 785	rel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen. Class: BAC ends. Location/Qualifiers 1. 1811 /organism="Pristionc/mol_type="genomic [/strain="California" /db xref="taxon:5412 /clone lib="Ppa Ecop/noce="The library with genomic DNA with vector."	An integrated physical and genetic map of the nematode Pristionchus pacificus Wol. Genet. Genomics 269 (5), 715-722 (2003) 22835951 22835951 Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemanustr. 37-39, Tuebingen D-72076, Germany	CG753732 1811 bp p048-4-G03.ya Ppa EcoRI BAC Librar genomic survey sequence. CG753732 CG753732.1 GI:37978509 GSS. Pristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chrc Neodiplogasteridae; Pristionchus. 1 (bases 1 to 1811) Srinivasan, J., Van der Meulen, M. and Buntjer, J., Van der Meulen, M. and
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hes 591; Conservative
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                 1053 АТАТТАРАТАРААТТАТТАРТАТАТАЛАРАРАРАДАТАРАДАТАРАТАРАТАРАТАРАТАРА
                                                    1720 ACATCCAACTAAGTATGTAACATATTACATAACAAACTTAAGTATAACTTAAAATTTCCT 1779
                                                                                                                                                               1480 AGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACC 1539
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/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
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/mol_type="genomic DNA"
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Suntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Neodiplogasteridae; Pristionchus.
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/note="The library was generated by a partial digest of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12916848.
                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                 AL565455

AL565455 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF005Y018 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                AL565455.2 GI:30549492
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2094 AATAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAACAATATGAAGAA 2153
                                                                                           2034 TCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCATTAGTTCTT 2093
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                                                                                                                                       Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9232.f For more information about this cluster, see http://www.genoscope.cns.fr/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Faraday Avenue Genoscope sequence ID : CS0DF005BH09NP1
                                                                                                                                                                                                                                GAĀĀTĀCCĀĀAĀCĀAACTTCTTAČTTCCČCTGTGGGTAĞGTĞCCACAGAATGAĀGAĞTĀĀ 377
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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/dev_stage="fetal"
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/db_xref="taxon:9606"
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/mol_type="mRNA"
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Local Similarity 39.2%;
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                                                           1218 TTGCATGTGGAATAATCGCTGGAAAAATTTAGGTAATAATGCTGTTGCTACTGTTATAA 1277
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
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1 (bases 1 to 1491)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.
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CG753221
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     CTAAAGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTTC 1337
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/clone_lib="Ppa_EcoRI_BAC_Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."
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/mol_type="genomic DNA"
/strain="California"
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2358 GAATTATATATATCTTCACCAACACATAGTTATCAAATTCTATAATACATCATATCCTTTT 2417
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1577 ATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCATCCTTTGATAATTT 1636
                                                           1277 ACTAAAGGCATGAATGAAATTAAAACACTATATATAGCAAAAAATCATTCAATAGATCTT 1336
                                                                                                                                                                                                                                                    1397 TCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATA 1456
                                                                                                                                                                                                                                                                                           1337 САТАСАТТААТТGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACAT 1396
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1 (bases 1 to 1348)

Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence. CG749499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371

Fax: 00497071601498
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Pristionchus pacificus
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GSS.
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                                                                                                   AAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAATTTATTACATGAGAAT 1576
                                                                                                                                                                         GATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTAGCA 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."
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/mol type="genomic DNA"
/strain="California"
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46.9%; Pred. No. 3.1e-11;
ative 0; Mismatches 616; Indels
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CG747831/c
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Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1376)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Ja
                                                                                                                                                                                       genomic survey sequence. CG747831
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                                                      1874 AAATAATATGTTTGCACACTTTTTCACTACATCATGTATATAATGAACATAATTTTACAT 1933
                                                                                                                                            1694 AAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATTACATAACA 1753
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
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Fax: 00497071601498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTA
                                                                                                    ААСТТААСТАТААСТТААААТТТССТАССТААТТАТАТАТАААСАААТТССТАТССТАТС 1813
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/clome_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
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/mol_type="genomic DNA"
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cgi-bin/cluster.cgi?seq=CS0CAP002BE04NP1&cluster=634.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0CAP002BE04NP1.
location/Qualifiers
                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 634.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX414736
BX414736 Homo sapiens THYMUS
3-PRIE, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                   Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1063)
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2265 AAATAATAAAGAAAAATCGTTATGTATATTTATACAATTACAAAATTTCCAACTTCAACA 2324
                                                                                                      2145 TATGAAGAAGATACAATACACGTCAAATAAATTAAACAAATTTCTAATATAACCACCTAC 2204
                                                                                                                                                                                                                                                                                                           2085 TTAGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAACAA 2144
                                                                                                                                                                                                                                                                                                                                                                                                                  2025 ATTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCA 2084
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/clone_Tib="Homo sapiens THYMUS"
/clone_Tibe="Homo sapiens THYMUS"
/note="Vector: pcWVSPORT 6; lst strand cDNA was primed
/note="Vector: pcWVSPORT 6; lst strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
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/db_xref="taxon:9606"
/clone="CSOCAP002Y108"
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Best Local Similarity 41.7%;
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     1556 ТАСААТТТАТТАСАТGАGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAG 1615
                                                                                                                                              1496 AAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATT 1555
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus
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                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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Pred. No. 8.6e-10;
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Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
1 (bases 1 to 1298)
                                                                                                          genomic survey sequence.
CG756607
CG756607.1 GI:37984341
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                                                   AGCTAATTATATAAACAAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATTA 1839
                                                                                                                 ACATCCAACTAAGTATGTAACATATTACATAACCAAACTTAAGTATAACTTAAAATTTCCT 1779
                                                                                                                                                                                                                                             АЛТТТGСАТАТСТАТТТАСАЛТТТАТТАСАТGAGAATATATCACTAGATAAAGCCATATC 1599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ralf.sommer@tuebingen.mpg.de
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/mol_type="genomic DNA"
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/clone_lib="Ppa EcoRI BAC Library"
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Pred. No. 9.3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 AAAAA 146
                                                                                                                                                          Max-Planck-Institute for Developmental Biolog Spemannstr. 37-39, Tuebingen D-72076, Germany
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CG749728
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P044-1-C03.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
                                                                                                Class: BAC ends
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                                                                                                                                                                                                          Contact: Sommer RJ
                                                                                                                                                                                                                                                                       pacificus
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Neodiplogasteridae; Pristionchus.
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                                                                                                          ralf.sommer@tuebingen.mpg
                  /mol_type="genomic DNA"
/strain="California"
   /db_xref="taxon:54126"
                                                organism="Pristionchus pacificus"
                                                                                location/Qualifiers
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Query Match Best Local

linear GSS 24-OCT-2003

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Matches 465; Conservative
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                                               2348 ACAAATTCAAGAATTATATATACTTCACCAACACATAGTTATCAAATTCTATAATACATC 2407
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TTACCCAAAAAGGTTAAAATACACATTCCTGCAACAATATGAAGAAGATACAATACACGT 2167
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/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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1 (Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.

Buntjer,J., van der Meulen,M. and Sommer,R.J.
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1288 bp DNA linear GSS 24-OCT-2003
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                Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
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                             1398 CACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAATAG 1457
                                                                                                    1338 ATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACATT 1397
                                                                                                                                                                          1278 СТАРАGGCATGRATGRAATTRARACACTATATATAGCARARARATCATTCAATAGATCTTC 1337
                                                                                                                                                                                                                                                                                                                      1158 TATACCATCAAGATATTATAGGTGTACAGATTGGAGCTGCATTAAAGAACATAATTGCAA 1217
                                                                                                                                                                                                                                                                                                                                                                                              1098 ATAATAAAGAACTTGGTGAATCATTGATAGAAACAATAAGTAATGATGTTCTAAAAATAA 1157
                                                                                                                                                                                                                                                1218 TIGCATGIGGAATAATCGCIGGAAAAATTIAGGIAATAATGCIGIIGCIACIGITATAA 1277
1 (bases 1 to 1434)
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC187638 1434 bp DNA linear GSS 08-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_line="UCD001, inbred 256"
/clone lib="CH261"
/clone lib="CH261"
/note="Vector: pTRRBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - For library and clone ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
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|sex="female"
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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1361 bp DNA linear GSS 24-OCT-200:
P036-4-E08.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic.
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Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."
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/mol_type="genomic DNA"
/strain="California"
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VERSION KEYWORDS RESULT 20 CG750869/c COMMENT REFERENCE SOURCE ORGANISM DEFINITION ACCESSION JOURNAL MEDLINE TITLE AUTHORS PUBMED Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J. An integrated physical and genetic map of the nematode Pristionchus CG750869 1373 bp DNA linea: P045~2-E10.za Ppa EcoRI BAC Library Pristionchus Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de Mol. Pristionchus pacificus Pristionchus pacificus genomic survey sequence CG750869 Class: BAC ends: 12884007 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. CG750869.1 GI:37972758 22835951 (bases 1 to 1373) Genet. Genomics 269 (5), 715-722 (2003) linear pacificus genomic, GSS 24-OCT-2003

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2260 GTATCAAATAATAAAGAAAAATCGTTATGTATATTTATACAATTACAAAATTTCCAACTT 2319
                                                      2140 ААСААТАТGААGAAGATACAATACACGTCAAATAAATTAAACAAATTTCTAATATATACCA 2199
                                                                                                                                                                                                                           2020 AATAAATTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTTAT 2079
                                                                                                                                                                                                                                                                                  1960 CATATATTAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACAT 2019
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                           GCCCATTAGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGC 2139
                                                                                                                                                                                                СТАСАТСАТСТАТАТАТААТGAACATAATTTTACATAAAATAACTAATAAAAAGAACCAATA 1959
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                                                                                                                                                                                                                                                                                                                                                                                                                                 the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
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source

High quality sequence stop: 418

Location/Qualifiers

organism="Dirofilaria immitis"

/dev_stage="adult" /lab_host="DH10B"

db_xref="taxon:6287"

/clone lib="Dirofilaria immitis adult pampi v1"
/note="Vector: pampi (Gibco); Site 1: Noti; Site 2: Sali;
/note="Vector: pampi (Gibco); Site 1: Noti; Site 2: Sali;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The CDNA was
made by using Dynabead oligo-dT priming (Dynal). PCR based
library using a modified protocol from the SMART PCR CDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of paMPI. Adult nemarcdes were harvested from
infected dogs by Dr. Prema Arasu of North Carolina State
University, Raleigh, NC (Prema_Arasu@ncsu.edu). Total RNA

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COMMENT
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The library was constructed by Claire Murphy and Dr. James McCarter
The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. Adult nematodes were harvested
from infected dogs by Dr. Prema Arasu of North Carolina State
from infected dogs by Dr. Prema Arasu@ncsu.edu) Total RNA was
isolated by Merry McLaird of Divergence, Inc., St. Louis, MO. DNA
Sequencing by: Washington University Genome Sequencing Center
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McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.

Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,

Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,

Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,

Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

The Mashington Univ. Nematode EST Project, 1999
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Seq primer: -40RP from Gibco
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Fax: 314 286 1810
                                                        Possible reversed clone: similarity
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Local Similarity 58.6%;
nes 214; Conservative (
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                                                                                                                                                                                                                                            Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pristionchus pacificus
Eukaryota; Metazoa; Nematoda, Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1297)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
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                                                                                                                                                                                                                                                                                                                                                                                                           ntegrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                   0049707160137
                                                                                                                                                                                                                                                                                                                                                                      Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                          ralf.sommer@tuebingen.mpg.de
/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db xref="caxon:54126"

/clone_lib="Ppa EcoRI BAC Library"

/note="The library was generated by a partial digest of
                                                                                                                                                    Location/Qualifiers
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Best Local Similarity 40.9%;
      2236 CTAAGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTATATTT 2295
                                                                                   2176 ТТАРАСБААТТТСТРАПТАТАЛАССАССТРСТСТРАДСАТАGGAACCAATAGTATATCATAC 2235
                                                                                                                                                                 2116 AAAGGTTAAAATACACATTCCTGCAACAATATGAAGAAGATACAATACACGTCAAATAAA 2175
                                                                                                                                                                                                                                              2056 AAATATGATAAACTGTTTTTTTATGCCCATTAGTTCTTAATAAAATTGCTAATTACCCAA 2115
                                                                                                                                                                                                                                                                                                                           1996 ААТАТТАСАТАGATGTCCTGACATAATAAATTCTATCATCCTTGACATATTTCAAACATA 2055
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                                                                           1736 СТААСАТАТТАСАТААСАААСТТААСТАТААСТТААААТТТССТАССТААТТАТАТАДАС 1795
   1616 ТСТАТСАТССТТТGАТААТТТСААСАСААТGАТАААТААСGGTCAAAAATATAGAATAC 1675
                                                                                                                                                                                                                                                                 1556 TACAATTTATTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAG 1615
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                                                                                                                                                                                                                                                                                                                                        270 АВАВЛАВАВАВЛЯЙАВАВЛИВЛЯВАВАНИЙВЙИЙДИВДЕВАДАВВАДАВВАДАВВАДЕВ 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1211)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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CG747324
CG747324.1 GI:37968250
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Pristionchus pacificus
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P040-4-D10.za Ppa EcoRI BAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                               h 2.6%; Score 122.8; DB 29; Length 1211; Similarity 39.9%; Fred. No. 3.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ralf.sommer@tuebingen.mpg.de
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/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
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/strain="California"
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Y Pristionchus pacificus genomic,
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                 Contact: Richard K. Wilson
Genome Sequencing Center
                                                                       1 (bases 1 to 1272)
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                       Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                               genomic survey sequence CC264939
Washington University School of Medicine
                                                       Unpublished (2003
                                                                                                                                                                                                                                                             CC264939.1 GI:30612358
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                                                                                                                                                                                                                                                                                                                                                                                                              2023 AAATTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTATGCC 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1903 CATCATGTATAATGAACATAATTTTACATAAATAACTAATAAAAAAGAACCAATACAT 1962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1783 ТААТТАТАТАДААСАААТТССТАТСТССТАТСТСААТТААССААТТGTTATCAGATTATAA 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1723 ТССААСТАА GTATGTAA CATATTA САТААСТАА СТАА СТТАА СТТАА АСТТАА АСТТССТА ССТАСТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1663 AAATATAGAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACA 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1604 ATATTATCTTAGTCTATCATCCTTTGATAATTTCAACA-CAATGATAAATAAACGGTCAA 1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  996
                                                                                                                                                                                                                                                                                                                                                                 Insert Lengt
Seq primer:
Class: BAC e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: (
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                         TCAAATAATAAAGAAAAATCGTTATGTATATTATACAATTACAAAATTTCCAACTTCAA 2322
                                                                                                                                    AATATGAAGAAGATACAATACACGTCAAATAAATTAAACAAATTTCTAATATAACCACCT 2202
                                                                                                                                                                                                                                                                         CATTAGTTCTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAAATACACATTCCTGCAAC 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATTAAATTACTAAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAAT 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     АТААСТСАААТТАААСТТТТАСТТАТТТАТААААТААТАТСТТТТСАСТА 1902
                                                                                                                                                                              .ass: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="CH261-19L17"
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/strain="Red Jungle Fowl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Gallus gallus"
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e_lib="CH261"
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CG753854/c
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Best Local Similarity
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1305 АЛАЛАЛИАЛАЛАЛИМИАДАЛАЛАЛАЛАЛАЛИМИКИЛАЛАЛАМИЛАЛАЛАМИЛАЛИ 1246
                                                                                                                                                                                                                                     1276 AACTAAAGGCATGAATGAAATTAAAACACTATATATATAGCAAAAAATCATTCAATAGATCT 1335
                                                                              1396 TTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTAAT 1455
                                                                                                                                                                                               1336 TCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAACA 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2443 CATAAATAATTATA 2456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2383 TAGTTATCAAATTCTATAATACATCATATCCTTTTTAAAAAGATGACTTCACAATTCATA 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2323 СААСААААСТСАААСТТСТАТТАТААСАААТТСААСААТТАТАТАТАСТТСАССААСАСА 2382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 TAATAATTATATTA 385
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Sommer RJ
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                                      AGATCACAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAAACCACTGATATCATTAGC 1515
                                                                                                                                                        (bases 1 to 1528)
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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Pred. No. 5e-09;
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ACCESSION
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P037-3-B03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
CG744812.1 GI:37965680
GSS.
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                                                                                                                                                                                                                           ANAAAANNNNNNNNNNACCACCATTCCAT 316
                                                                                                                                                                                                                                                                                                                 AAGAATTATATATACTTCACCAACACACATAGTTATCAAATTCTATAATACATCATATCCTT 2415
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  1959 ACATATATTAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACA 2018
                                                                                                                                                                                                                                                                    1779 TAGCTAATTATATAAACAAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATT 1838
                                                                                                                                                                                                                                                                                                                                                                                                      1839 ATAAATAAGTCAAATTAAACTTTTTACTTATTTATAAAATAATATGTTTGCACACTTTTTC 1898
                                                                                                                                                                                                                                                                                                                                                         1719 ААСАТССААСТААСТАТСТААСАТАТТАСАТААСАААСТТААСТАААСТТААААТТТСС 1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                1659 TCAAAAATATAGAATACAACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTT 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1600 AAACATATTATCTTAGTCTATCATCCTTTGATAATTT-CAACACAATGATAAATAAACGG 1658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1420 AGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGA 1479
                                                                                                                                                                                                                                                                                                                 Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Pristionchus pacificus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ralf.sommer@tuebingen.mpg
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Neodiplogasteridae; Pristionchus.
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/mol_type="genomic DNA"
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/clone_lib="ppa EcoRI BAC Library"
note="The library was generated by a partial digest of
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/strain="California"
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                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
                                                                                                                                                                                                                                       Seq primer: RM1 TACGACTCACTATAGGGAGAC1ass: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                          Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC253231 1277 bp DNA linear GBS 13-WAI-200 CH261-180N11_RM1.1 CH261 Gailus gallus genomic clone CH261-180N11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformés; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence CC253231
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                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2003)
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                                                                                                                                                                                               quality sequence start: 24 quality sequence stop: 85.
/sex="female"
/cell_line="UCD001, inbred
/clone_lib="CH261"
                                                            /clone="CH261-180N11"
                                                                                             organism="Gallus gallus"

/mol_type="genomic_DNA"

/strain="Red_Jungle_Fowl"
                                                                                                                                                                            location/Qualifiers
                                                                                 xref="taxon:9031"
                        256"
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OY 1335 TTCATACATTAATTGGTCCATCATGTCTAGGAGATCTAATATTAACATGAACAGGAAC 1394 Db 1363 TAAAAANNTANAAANAAAAAAAAAAAAAAAAAAAAAAA	Query Match 2.5%; Score 120.2; DB 29; Length 1433; Best Local Similarity 41.4%; Pred. No. 8.9e-09; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Pred. No. 8.9e-09; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Pred. No. 8.9e-09; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Pred. No. 8.9e-09; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Pred. No. 8.9e-09; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Pred. No. 8.9e-09; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Pred. No. 8.9e-09; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 646; Indels 1; Gaps 1; Matches 457; Conservative 0; Mismatches 1; Gaps	Class: BAC ends. Location/Qualifiers 1. 1433 Location/Qualifiers 1. 1433 /mol_type="Pristionchus pacificus" /strain="California" /strain="California" /db_xref="taxon:54126" /clone_lib="Ppa EcoRI BAC Library" /note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."	net Genomics 269 (5), 31 31 32 33 33 34 35 35 37 37 38 38 38 38 39 39 39 39 39 39 39 39 39 39 39 39 39	KEYWORDS GSS. SOURCE Pristionchus pacificus ORGANISM Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. REFERENCE 1 (bases 1 to 1433) AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J. An integrated physical and genetic map of the nematode Pristionchus	N 0N /c	OY 2388 ATCAAATTCTATAATACATCCTTTTTAAAAAGATGACTTCACAATTCATAACATAA 2447
RESULT 29 CG750135 CG750135 CG750135 CG750135 CG750135 CG750135 DEFINITION P0443-D09.za Ppa EcoRI EAC Library Pristionchus pacificus genomic, genomic survey sequence. ACCESSION CG750135 VERSION CG750135.1 GI:37971278 KEYWORDS GSS. SOURCE Pristionchus pacificus Pristionchus pacificus Eukaryota; Medazoa, Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. REFERENCE 1 (base 1 to 1592) AUTHORS Buntjer,J., van der Meulen,M. and Sommer,R.J. TITLE An integrated physical and genetic map of the nematode Pristionchus	Qy 2294 TTATACAATTACAAAATTTCCAACATCAACAACAAAACTCAAAGTTCTATTATAACAAAA 2353	Oy 2114 AAAAAGTTAAAATACACATTCCTGCAACAATATGAAGAAAAAAAA	Db 763 AAAAAAANAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Оу 1814 ТСААТТААССДАТТӨТТАГСАGАТТАТААДТААДТААДТАТАДАСТТТТАДАСТТАТТАГА 1873	1694 AAAAAGCAGTCAAATACCGATCGTTAACATCCCAACTAAGTATGTAACATATTACATAACA	OY 1574 AATATATCACTAGATAAAGCATATCAAACATATTATCTTAGTCTATCATCATGATAA 1633

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                                                     2020 ААТАААТТСТАТСАТССТТGАСАТАТТТСАААСАТААААТАТGАТАААСТGTTTTTTTAT 2079
                                                                                                                                                                    1900 СТАСАТСАТСТАТАТААТСААСАТААТТТТАСАТАААТЛАСТААТААААСААССААТА 1959
                                                                                                                                                                                                                             1840 TAAATAAGTCAAATTAAACTTTTACTTATTTATAAAATAATATGTTTGCACACTTTTTCA 1899
                                                                                                                                                                                                                                                                                      1780 AGCTAATTATATAAACAAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATTA 1839
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Similarity 42.2%;
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076; Germany
Tel: 00497071601371
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GCCCATTAGTTCTTAATAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGC 2139
                           TANATAATAATTTATTAATTTTTATTAAAATAATTTTNATATTÄTAANATTTATTAAATT
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/mol_type="genomic DNA"
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Fax: 520 621 9288
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PCR PRimers
PCRWARD: atc agc ggc cgc gat cc
PCRWARD: gta aaa cga cgg cca gtg
PCRWARD: gta aaa cga cgc gat cc
                                                                                                              Plate: 0091 row: G column: 12
Seq primer: atc agc ggc cgc gat cc
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                              Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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Sorghum propinquum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Liliopsida, Poales, Poaceae, PACCAD
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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Wing,R., Yu,Y., Kim,H.R., Collura,K., Pries,G.,
Soderlund,C. and Harfield,J.
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BZ696936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing of Sorghum BAC ends. http://genome.arizona.edu/stc/sorghum
                                                                                                                                                                                                                                                                           Email: http://genome.arizona.edu
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/mol_type="genomic DNA"
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2304 ACAAAATTTCCAACTACAACAACAAACTCAAAAGTTCTATTATAACAAATTCAAGAATTA 2363
                                                                                                                                           2184 ATTTCTAATATAACCACCTACTCTAAACATAGGAACCAATAGTATATCATACCTAAGTAA 2243
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                                                                              2244 GATATCCCTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTATATATTTATACAATT
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                                                                                                              АТАААА БАДОТАТАСАТАТТАРААТТАСТАВАА САССТАТТТАСТАССТАВТАТТАС 2003
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/clone_Tib="SP_Ba"
/clone_Tib="SP_Ba"
/notee="Vetor: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Paterson lab BAC library (HindIII)"
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/clone="SP__Ba0091G12"
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                                                                                                                                                                                                                                                                                                                               1849 CAAATTAAACTITTACTTATTATAAAATAATATGTTTGCACACTTTTTCACTACATCAT 1908
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  2029 TATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCATTAG 2088
                                                                                                                                                                                                                     1909 GTATATAATGAACATAATTTTACATAAAATAACTAATAAAAAGAACCAATACATATATTA 1968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNSOOEVL 1101 bp DNA linear GSS 04-JUN-1: Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (02-UNM-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                       AATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATAAATTC 2028
                                                                                                                                                                                                                                                                             МММММНАМАТУТСТСАНТИТММММИМИМААТИТИМАЛАМАЛАМТТАТИВАТИВАЛАМА 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db xref="taxon: 7227"
/clone="BACR29B23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-98"
/note="end : T7"
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Pred. No. 1.3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2448 ATAATTATACATGCAATGTTTATTCAGAAACATTACACAATCCAAGAATTTTCAATTTA 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2389 TCAAATTCTATAATACATCATAT-CCTTTTTAAAAAGATGACTTCACAATTCATACATAA 2447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG749971 1377 bp DNA linear GSS 24-OCT-200: P044-2-E09.za Ppa EcoRI BAC Library Pristionchus pacificus genomic.
                                                                                                                                                                                                                                                                                   Evolutionary Biology
Max-Planck Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
1 (bases 1 to 1377)
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                                                                                                                                                                                                                                               ralf.sommer@tuebingen.mpg
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                                                                   /clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                                        /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                           db_xref="taxon:54126"
 2.5%;
 Score 119.4;
   DB 29;
 Length 1377;
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 2294 TIATACAATTACAAAATITCCAACTICAACAACAAACTCAAAGTTCTATTATAACAAAT 2353
                                                                                         2234 ACCTAAGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAAAAATCGTTATGTATAT 2293
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                                                        AATTAAACAAATTTCTAATATAACCACCTACTCTAAACATAGGAACCAATAGTATATCAT 2233
                                                                                                                                                                                                                                AAAAAGGTTAAAATACACATTCCTGCAACAATATGAAGAAGATACAATACACGTCAAATA 2173
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Best Local Similarity
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                                       1744 TTACATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAAAAATTCCT 1803
                                                                                                                          1684 CCACATATATAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATA 1743
                                                                                                                                                                  1624 CCTTTGATAATTTCAACACAATGATAAATAAACGGTCAAAAATATAGAATACAACGTTCA 1683
                                                                                                                                                                                                                                                   1564 ATTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTATCAT 1623
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      941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP001AB01QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 1124)
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BX436282 Homo sapiens THYMUS
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<u> ҰҰҰҰҰҰĀĀĀĀĀĀĀĀĀĀĀAНМАĀĀҰҰҰҰННҰНҰҰҰҰҰҰДĀĀĀĀĀĀĀĀĀĀҰҰҰҰҰҰ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="CS0CAP001YC01"
/tissue_type="THYNUS"
/clone_lib="Homo sapiens THYNUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               2.5%; Score 117.8; DB 13; Length 1124; 27.1%; Pred. No. 2.2e-08; Indels 16; Gaps
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sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2031 ТСАТССТТGАСАТАТТТСАААСАТААААТАТGАТАААСТGTTTTTTTTATGCCCATTAGTT 2090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        761 МНҮНАЛАЛАЛАЛАЛАНҮҮҮҮЛДАЛАЛАЛАЛАННАЛАЛАЛАЛАЛАЛАНҮНАЛАЛАЛАЛАЛАНҮҮҮ 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1426)
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
Unpublished (2003)
                                                                              High quality sequence start: 276 High quality sequence stop: 339.
                                                                                                                      Seq primer: RM1 TACGACTCACTATAGGGAGA Class: BAC ends
                                                                                                                                                             Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: (
                                                                                                                                                                                                       Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC231597 1426 by CH261-36A19_RM1.1 CH261 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS
                                                                                                                                                                                                                                                Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC231597.1 GI:30558260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTAATAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAACAATATGAA 2150
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/mol_type="genomic DNA"
                   organism="Gallus gallus"
                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1426 bp
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gallus genomic clone CH261-36A19,
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ORIGIN

Query Match

489

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Matches 416;
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                            2218 ACCAATAGTATATCATACCTAAGTAAGATATCCCTACAGCATGTATCAAATAATAAAGAA 2277
                                                                                                                                                                                                                     2098 AAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGCAACAATATGAAGAAGATA 2157
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                                                                                                                     2158 CAATACACGTCAAATAAATTAAACAAATTTCTAATATAACCACCTACTCTAAACATAGGA 2217
                                                                                                                                                                                                                                                                                                              2038 TGACATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCATTAGTTCTTAATA 2097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1918 GAACATAATTTTACATAAAATAACTAATAAAAAGAACCAATACATATATTAAATTACTAA 1977
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                                                                                                                                                                        728 АЛАРАНАНАЛАРАВА АНАНАРАЛАНАЛАРАЛАРАВА В АДАРАВАНАРАНАЛАЛАРАДАЛА 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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/clone lib="CH261"
/clone lib="CH261"
/note="Vector: pERBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-36A19"
/sex="female"
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                                                                       1454 ATAGATCACCAACCTAAAGCTTGTTGAAGGAACCAGTACTGTAAAACCACTGATATCATTA 1513
                                                                                                                                                                                                                                                                   1334 CTTCATACATTAATTGGTCCATCATGTCTTGGAGATCTAATATTAACATGTACAACAGAA 1393
                                                                                                                                                                                                                                                                                                                                                               1274 АТААСТАААGGCATGAATGAAATTAAAACACTATATATATAGCAAAAAATCATTCAATAGAT 1333
                                                                                                                                                                     1394 CATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAAGGTAGAAATATAAATACATTA 1453
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 1001 High quality sequence stop: 1061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: RM1 TACGACTCACTATAGGGAGA Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Richard K. Wilson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site_2: EcoRI; CH261 Female Chicken library - for library and clone ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_line="UCD001, inbred 256"
/clone_lib="CH261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="temale"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Red Jungle Fowl"
/db_xref="taxon:9031"
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708794 of library G from Tetracdon nigroviridis, genomic survey
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                                           1807 TCCTATCTCAATTAACCAATTGTTATCAGATTATAAAATAAGTCAAATTAAAACTTTTACTT 1866
                                                                                                                                      1747 CATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACAAATTCCTATC 1806
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                                                                                                                                                                                                                              1687 САТАТАТАААААGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATGTAACATATTA 1746
                                                                                                                                                                                                                                                                                                                      1627 ТТGATAATTTCAACACAATGATAAATAAACGGTCAAAAATATAGAATACAACGTTCACCA 1686
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                                                                                          429;
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-APR-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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45.5%; Pred. No. 2.9e-08;
tive 15; Mismatches 488;
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                           Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., BuntJer,J., van der Meulen,M. and Sommer,R.J. An integrated physical and genetic map of the nematode Pristionchus
                                                                                         Email: ralt.somm Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
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                                                                                                                    ralf.sommer@tuebingen.mpg
organism="Pristionchus pacificus"
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/strain="California"
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Qy 1375 ATTAACATGTACAACAGAACATTCACGCAATATGGCTTTTGGACTAGAAATAGGAAAGG 1434	ORIGIN Query Match Best Local Similarity 46.6%; Pred. No. 3.7e-08; Matches 487; Conservative 0; Mismatches 542; Indels 15; Gaps 5;	.mpg.de chus pacificus" NAA" 26" 26 "	MEDLINE 22835951 MEDLINE 22835951 PUBMED 12884007 COMMENT Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601378	GSS. GSS. Pristionchus pacificus Pristionchus pacificus Elkaryota; Metazoa; Nematoda; Chromado Neodiplogasteridae; Pristionchus. 1 (bases 1 to 1592) Srinivasan, J., Sinz, W., Jesse, T., Wigg Buntjer, J., van der Meulen, M. and Somm An integrated physical and genetic map pacificus	CG750135/C CG750135 DEFINITION P044-3-D09.Za Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence. ACCESSION CG750135 CG750135 CT.2007177	Qy 2393 ATTCTATAATA 2403 	Oy 2333 CAAAGTTCTATTATAACAAATTCAAGAATTATATATATACCACCAACACATAGTTATCAA 2392 Oy 230 CAAAGTTCTATTATAACAAATTCAAGAATTATATATATACCAACACACAC	73 AAGAAAAATCGTTATGTATATTATACAATTACAAAATTTCCAACTTCAACAACAAAACT
RESULT 39 EX437039 EACCUS DEFINITION BX437039 EACCESSION BX437039 VERSION EXT. SOURCE Homo sapiens (human) ORGANISM	Oy 2394 TICTADAAAATTTTANTTTAT 2417 Oy 2394 TICTADAAAATTTTANTTTATTATAATAAAATAAAATAAAAAAAA	2215 GGAACCA-ATAGTATATCATACCTAAGTAAGATATCCCTACAGCATGTATCAAATAATAA 759 ATAATTAATTATTATTATTATTATAAAATATTTAATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAA	Db 938 TATT-ATATTATATATATATATAAAAATTATAAATNATAAAAATTAATAA	1915 AATGAACATAATTTTACATAAAATAACTAATAAAAGAACCAATACATATATAATTAC	QY 1795 CAAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATTATAAATAA	Qy 1735 TGTAACATATTACATAACATAACTTAAGTATAAAATTTTCCTAGCTAATTATATAAA 1794	OD 1555 AIAIAITAAITTAAITTAAITTAIAITTIAAIANIAIAIAAAAAITAIAAIAAIAAIAAIAAIAAIAAIAAIAA	1615 GTCTATCATCCTTTGATAATTTTCAACACAATGATAAATAA

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                    2097 АЛЛАТТЭСТЛАТТАСССАЛАЛАGGTTAAAATACACATTCCTGCAACAATATGAAGAAGAT 2156
                                                                                                                                                                                                                                                                                                              1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1561 TTTATTACATGAGAATATATCACTAGATAAAGCCATATCAAACATATTATCTTAGTCTAT 1620
                                                                                                                   2037 TTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTTATGCCCATTAGTTCTTAAT 2096
                                                                                                                                                                                                                                                                                                                                                                                                         1857 ACTTTTACTTATTATAAAATAATATGTTTGCACACTTTTTCACTACATCATGTATATAA 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1737 TAACATATTACATAACAAACTTAAGTATAACTTAAAATTTCCTAGCTAATTATATAAACA 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1621 CATCCTTTGATA----ATTTCAACACAATGATAAATTAAACGGTCAAAAATATAGAATACA 1676
                                                                                                                                                                                                                                                              759 ТАТАТАЛАТАТИТААЛАТААМААЛААТЛАТТАААМТААҮДАЛАДТАДИТТААДАТДАТА 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      579 AAAAAAAAAAAWATTAAATWTTTAAATÄAATAAATATTTTWÄAAAAAWTAAATATATA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7009.f For
nore information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgi-bin/cluster.cgi?seq=CSOCAP004DD02QP1&cluster=7009.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Faraday Avenue Genoscope sequence ID : CS0CAP004DD02QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genoscope.cns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 42.4
97; Conservative
                                                                         CAMAATATATCAAACACWATAMAAACAAWAACWCATHAAMTCTCAAATWTYTWWTWYYYY 938
                                                                                                                                                                                                                   AAACACCTATTTACTACGTAATATTACATAGATGTCCTGACATAATAAATTCTATCATCC 2036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGTTCACCACATATATAAAAAGCAGTCAAATACCCATCGTTAACATCCAACTAAGTATG 1736
                                                                                                                                                                      AAAAATAAAAATÄAAWATAÄATANAÄTNTÄATATTATNATWCATTTÄTÄATAATCACÄAAA 878
                                                                                                                                                                                                                                                                                                           ТGAACATAATTTTACATAAAATAACTAATAAAAAAGAACCAATACATATATTAAATTACTA 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTTAWTTAAAAAWTATTTAAAATAWATAAAAATTAWATAAAAAYTAAAAYTAAAAWTAWTAAA 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACCAATTTGCATATCTATTTACAA 1560
                                                                                                                                                                                                                                                                                                                                                           AAAATATATAAWTWAAAAAAATAWATATINTTATAAWATATAANAAAATNTAWAWTWA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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'clone="CS0CAP004YH04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.4%; Score 115.8; DB 13; Length 1061;
42.4%; Pred. No. 4.5e-08;
7ative 56; Mismatches 343; Indels 4;
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG744200/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                    1720 АСАТССААСТАЯСТАТСТААСАТАТТАСАТААСАЛАСТТААСТАТААСТТАААТТТССТ 1779
                                                                                                                   1660 CAAAAATATAGAATACAACGTTCACCACATATATAAAAAAGCAGTCAAATACCCATCGTTA 1719
                                                                                                                                                                                                              1480 AGGAACCAGTACTGTAAAACCACTGATATCATTAGCAAAAAAACTTAATGTAGAACTACC 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1420 AGAAATAGGAAAAGGTAGAAATATAAATACATTAATAGATCACAACCTAAAGCTTGTTGA 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               939 ҮҮТҮТҮТТТҮТМТАҮАМААААСААААААҰАААҰАМАҰАСАМААААААААСААСМАТАТ 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1305)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG744200 1305 bp DNA linear GSS 24-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evolutionary Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSD
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CG744200.1 GI:37965068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pristionchus pacificus
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                                                                      AATTTGCATATCTATTTACAATTTATTACATGAGAATATATCACTAGATAAAGCCATATC 1599
                                                                                                                                                                                                                                                                                                                                                           ACATATCTAYNMACTMAAAACAAAAAAYATWTAAACWAAA 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:54126"
/clome_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 115.6; DB Pred. No. 4.5e-08
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Gaps

	1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	451	
	O GTATCAAATAATAAGAAAAATCGTTATGTATATTTATACAATTACAAAA 2309	2260	`
452	<u> </u>	511	U
2259	CCTACTCTAAACATAGGAACCAATAGTATATCATACCTAAGTAAG	2200	
512	алаланалалалалалалалалалалалалалалалала	571	U
2199	AACAATATGAAGAAGATACAAGTCAAATAAATTAAACAAATTTCTAATATATAACCA	2140	_
572	NANDAAAAANNAAAAAAAAAAAAAAAAAAAAAAAAAAAA	631	Ü
2139	O GCCCATTAGTTCTTAAAAATTGCTAATTACCCAAAAAGGTTAAAATACACATTCCTGC 2139	2080	`
632		691	Ü
2079	AATAAATTCTATCATCCTTGACATATTTCAAACATAAAATATGATAAACTGTTTTTTAT	2020	,
692	1 дааалдаалдаалдаалаалаалаалаалаалаалаалаа	751	Ü
2019	CATATATAAATTACTAAAACACCTATTTACTACGTAATATTACATAGATGTCCTGACAT	1960	•
752	анадалаланалалалалалалалалалалалалалалал	811	Ü
1959	CTACATCATGTATATAATGAACATAATTTTACATAAAATAACTAATAAAAAAGAACCAATA	1900	`
812	1 да а а а а а а а а а а а а а а а а а а	. 871	Ü
1899	TAAATAAGTCAAATTAAACTTTTACTTATTATAAAATAATATGTTTGCACACTTTTTCA	1840	`
872	ARAAAAAAAAAAAANANANANANAAAAAAAAAAAAAAA	931	U
1839	AGCTAATTATATAAACAAATTCCTATCTCCTATCTCAATTAACCAATTGTTATCAGATTA	1780	_
932	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	991	O

Search completed: April 5, 2004, 21:30:39 Job time: 11174 secs